ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA

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Submitted By

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Dedicated

to

my Family

&

Teachers

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Dr. Yuvika Saini

LIST OF ABBREVIATIONS

ARDS	Acute Respiratory Distress Syndrome
ATS	American Thoracic Society
BA	Bronchial Asthma
BAL	Bronchoalveolar Lavage
CAD	Coronary Artery Disease
CAP	Community Acquired Pneumonia
CBC	Complete Blood Count
CFU	Colony Forming Units
CKD	Chronic Kidney Disease
COPD	Chronic Obstructive Pulmonary Disease
CS	Culture Sensitivity
CTX-M	Cefotaxime-Munich
CVA	Cerebrovascular Accident
DAMA	Discharge Against Medical Advice
DM	Diabetes Mellitus
ET	Endotracheal Tube
FA	Film Array
GNC/GNB	Gram negative cocci/gram negative bacilli
GPC/GPB	Gram positive cocci/gram positive bacilli
HAP	Hospital Acquired Pneumonia
HTN	Hypertension
ICU/CCU	Intensive Care Unit/Critical Care Unit
IDSA	Infectious Disease Society of America
ILD	Interstitial Lung Disease
IMP	Imipenemase
KPC	Klebsiella Pneumoniae Carbapenemase
LBBB	Left Bundle Branch Block
LFT	Liver Function Tests
LRTI	Lower Respiratory Tract Infections
NDM	New Delhi Metallobetalactamase
NIV	Non-Invasive Ventilation
NVBS	Normal Vesicular Breath Sounds
PCR	Polymerase Chain Reaction
PP	Pneumonia Panel
RA	Room air

RFT	Renal Function Tests
VAP	Ventilator Acquired Pneumonia
VIM	Verona Imipenemase

ABSTRACT

INTRODUCTION: Pneumonia, a significant and acute respiratory infection, affects the lung parenchyma, alveoli and the distal airways. It poses a considerable health challenge globally, associated with high morbidity and mortality rates across all ages. Pneumonia is categorized into community-acquired pneumonia, contracted outside hospital settings, and hospital-acquired pneumonia and ventilator acquired pneumonia which occurs after 72 hours of hospitalisation and mechanical intubation respectively.

AIM & OBJECTIVES: 1) To compare the clinical significance of diagnosing Pneumonia using the FilmArray method versus standard diagnostic methods. 2) To assess the differences in clinical cure rates of Pneumonia between patients treated based on FilmArray test results and those treated with standard methods. 3) To evaluate the improvement in antimicrobial selection for Pneumonia patients treated according to FilmArray test results versus standard treatments.

METHODOLOGY: This study utilized clinical specimens from 83 hospitalized patients at DMCH Ludhiana, including sputum, ET secretions and BAL. These samples were analyzed using a multiplex real-time PCR assay. Standard methods involved gram stain and culture sensitivity testing of sputum samples. The study included hospitalized patients showing signs of pneumonia.

RESULTS AND CONCLUSION: The study found a predominant patient age group of 50-69 years, there was a higher prevalence of male, most common complaints were dyspnea. The overall sensitivity and specificity of FA for bacterial targets was 72.2% and 92% respectively and 93% specificity for viral targets. Clinical and radiological improvements were observed in nearly half of the patients, demonstrating the efficacy of the treatments used.

Keywords: Randomised controlled trial, CAP, HAP, VAP, FilmArray; multiplexed BioFire PP; genetic markers; antibiotic sensitivity

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INTRODUCTION

Pneumonia, a common acute respiratory infection, affects the lung parenchyma, alveoli, and distal airways. It is a significant health issue associated with high morbidity and short- and long-term mortality across all age groups globally. Pneumonia is categorized as community-acquired or hospital-acquired. Hospital-acquired pneumonia (HAP) is defined as pneumonia occurring 48 hours or more after hospital admission and not present at the time of admission.[1] Ventilator-associated pneumonia (VAP) is a notable subset of HAP that occurs in intensive care units (ICUs). It can lead to mild to life-threatening illness in individuals of all ages and is the largest infectious cause of death in children worldwide. This differentiation is critical because it affects the treatment and management approach for the disease. Pneumonia poses a significant global health challenge and is a leading cause of illness and death across all age groups. Community-acquired pneumonia (CAP) is a major contributor to global mortality and morbidity. India contributes to 23 percent of the global pneumonia burden.[2] The outlook deteriorates as comorbidities accumulate and when medium and high-risk comorbidities are combined. Patients with CAP and high-risk comorbidities had a higher chance of being transferred to the ICU.[3] Despite these concerning statistics, advancements in the rapid and accurate identification of causative agents and the timely initiation of appropriate therapies have resulted in a noticeable decrease in morbidity and lower mortality rates.

The BioFire FilmArray Pneumonia Panel plus (BFPP) represents a significant advancement in diagnostic technology, especially in the field of lower respiratory tract infections. This innovative system utilizes a multiplexed PCR technique that involves sample preparation, nucleic acid extraction, amplification, and pathogen analysis, all completed within about an hour. While early multiplexed molecular assays were initially intended for detecting upper respiratory pathogens, many labs have tested these assays to analyze lower respiratory samples.[4]

Compared to traditional culture techniques, this method is distinguished by its simplicity and effectiveness. Additionally, BFPP is capable of simultaneously identifying the most common pathogens responsible for pneumonia, thereby improving the speed and precision of diagnosis for this condition.[5]

Identifying the specific infectious cause of pneumonia in patients has been associated with a significant reduction in mortality rates, likely due to the ability to provide targeted and effective therapy. Traditionally, laboratory diagnosis of lower respiratory tract infections, including pneumonia, has heavily depended on quantitative and qualitative bacterial cultures. While these methods are crucial for determining appropriate antibiotic treatment, their effectiveness can be hindered by various factors such as prior antibiotic exposure, the demanding nature of some pathogens, or the overgrowth of local flora.[6] Many unnecessary antibiotics are prescribed, especially for viral infections, which results in an increased pill burden and gives rise to resistant strains. Approximately 2.8 million people worldwide are affected each year, and there are 35,000 annual deaths.[7] As a result, methods based on culture frequently produce inconsistent outcomes and necessitate turnaround times of 48 hours or longer. Furthermore, extra tests, such as specific cultures or molecular assays, might be needed to identify unusual bacteria or viral pathogens, which clinicians may not routinely ask for. These restrictions together reduce the effectiveness of current standard-of-care techniques to promptly and precisely pinpoint infectious causes and customize antibiotic treatment accordingly.[8]

On the other hand, molecular diagnostics, especially PCR-based tests, present a quick and precise option, delivering results within hours of collecting the specimen. These tests have the capability to considerably reduce the length of broad-spectrum empirical antibiotic treatment by detecting pathogens or particular antibiotic resistance

markers much earlier than traditional methods, possibly by 2 to 3 days.[9]

HAP and VAP are commonly seen in seriously ill and critical patients. Failure to diagnose promptly can result in significant sickness and fatalities. Excessive use of powerful antibiotics can lead to resistance to them. Clinical and radiological diagnosis is performed as part of the regular procedure. Molecular methods, involving invasive techniques such as BAL and brush specimen, have facilitated early diagnosis, optimal antibiotic choices, and proper use of powerful antibiotics, as compared to traditional microbial techniques. This has also decreased unnecessary exposure to drugs.[10]

Rationale of the study-

The frequency and consequences of pneumonia require improvements in diagnostic techniques that not only increase the accuracy of diagnoses but also guide appropriate antibiotic treatment, ultimately impacting patient results. While traditional culture methods are thorough, they often take a long time to produce results, potentially delaying critical interventions. The introduction of multiplex PCR Pneumonia Panels provides a promising option. This technology allows for the quick identification of a broad spectrum of pathogens responsible for pneumonia, significantly decreasing the time from presentation to diagnosis. By offering timely and accurate pathogen detection, these panels facilitate targeted antibiotic selection, which is essential in the era of rising antibiotic resistance. This study seeks to assess the effectiveness of multiplex PCR Pneumonia Panels in diagnosing pneumonia, guiding antibiotic selections, and enhancing clinical outcomes, potentially transforming the management of this common yet serious illness.

AIMS AND OBJECTIVES

- To compare the clinical significance of diagnosing Pneumonia in patients with Film Array versus those with standard methods.
- To determine whether there is an improvement in antimicrobial selection in Pneumonia patients treated according to the Film Array test versus those treated with standard methods.
- To determine any difference in clinical cure of Pneumonia between patients treated according to the Film Array test's molecular results versus those treated with standard methods.

REVIEW OF LITERATURE

Pneumonia is a significant global health concern that causes a substantial amount of sickness and death. India, in particular, is confronted with a significant portion of the world's pneumonia problem, representing about 23 per cent of all cases. The mortality rates for these cases vary widely, with reported fatality rates ranging from 14 to 30 per cent. The prevalence of *Streptococcus pneumoniae* is a major contributing factor to these high rates, as it is identified as the primary bacterial cause of pneumonia, followed by *Burkholderia pseudomallei*.[2] This highlights the critical need for effective management and treatment strategies to combat this pervasive health threat, particularly in regions with high incidence rates.

Conventional microbiological diagnosis-

It is crucial to thoroughly evaluate the microbiology for patients diagnosed with pneumonia. This usually involves performing a sputum culture, a urinary antigen test to detect *Streptococcus pneumoniae* and *Legionella pneumophila*, and a blood culture. Additionally, serological testing may be conducted to identify atypical bacterial pathogens. Studies show that an underlying cause can be determined in about 53% to 75% of cases with intensive microbiological testing, with *Streptococcus pneumoniae, Mycoplasma pneumoniae*, and *Haemophilus influenzae* being the most commonly identified pathogens. The diagnostic effectiveness of routine cultures in community-acquired pneumonia is limited, with an incidence ranging from 0 to 14% across 13 studies, and their usefulness in identifying resistant pathogens that would require broadening antibiotic therapy is even lower, involving fewer than 1% of patients. While routine blood cultures in community-acquired pneumonia are now considered to have low value and are no longer recommended by current IDSA/ATS guidelines, the role of blood cultures in severe community-acquired pneumonia and in healthcare-associated pneumonia remains uncertain.[11-13]

Moreover, Pleural effusions frequently occur in individuals who contract pneumonia. Approximately 40-60% of patients with bacterial pneumonia will experience a pleural effusion of different levels of severity. Around 20% to 40% of hospitalized pneumonia patients will develop parapneumonic effusion.[14]

The specificity of pleural exudates culture analysis is high, while its sensitivity is limited due to the rare occurrence of infections penetrating the pleura. The Gram stain of pleural exudates demonstrates different levels of sensitivity, with rates around 80% for pneumococcal pneumonia and 78% for staphylococcal pneumonia, and a specificity ranging from 93% to 96%. These methods and processes for diagnosis are essential for accurately identifying the causative agents, guiding effective treatment approaches, and ultimately improving patient outcomes.[14]

DETECTION USING PCR

BIOFIRE PN Panel, detects 33 targets, including eight viruses, 18 bacteria, and seven antimicrobial resistance genes associated with lower respiratory tract infections.

Sample Type
BAL-like: (including mini-BAL)
Sputum: (including endotracheal aspirate)

Performance
BAL-like: 96% sensitivity and 98.3% specificity
Sputum: 96.3% sensitivity and 97.2% specificity

PCR's ability to detect micro-organisms provides substantial benefits for diagnosing pneumonia, mainly because of its quick processing time and decreased reliance on bacterial viability. In contrast to conventional cultures which require live bacteria, PCR has the capability to identify DNA fragments, allowing it to remain effective

even after the start of antibiotic treatment. For instance, **Johansson et al.**[15] observed that in a group of 184 patients with pneumonia, 80% of those who tested positive for *S. pneumoniae* using PCR but had negative sputum cultures had been administered antibiotics prior to the collection of sputum samples. This highlights the value of PCR in medical environments where patients are frequently treated with antibiotics, which may compromise culture techniques.

Research has shown that genes that encode pneumolysin (ply), autolysin (lytA), pneumococcal surface adhesion A (psaA), penicillin-binding protein, and manganese-dependent superoxide dismutase have been utilized for identifying *S. pneumoniae* through PCR-based tests. The primary targets for detecting *S. pneumoniae* are the ply and lytA genes. Even though lytA is found in *S. pneumoniae* and similar species like oral streptococci, the lytA gene displays enough variation that appropriately designed primers can specifically identify *S. pneumoniae*[16,17]

The frequency of respiratory tract infections from *S. pneumoniae* and *H. influenzae* has decreased following the introduction of vaccination programs for older adults and children. Moreover, differences may have stemmed from the finicky characteristics of *H. influenzae*, which is challenging to culture.[18,19]

Diagnosing *L. pneumophilia* is challenging using serology and culture techniques, but much simpler with FilmArray PP. Detecting *Legionella* infection has been restricted by challenges in growing the bacteria and the non-specific nature of serological tests, which can only identify *L. pneumophila* serogroup 1 and not the other species and serogroups.[20,21]

The Unyvero platform is a rapid diagnostic system that uses multiplex PCR (M-PCR) for the microbiological diagnosis of severe infections within 5 hours. The Unyvero Hospitalised pneumonia M-PCR panel identifies 21 bacteria associated with CAP and HAP, including most of

the *Enterobacterales, Pseudomonas aeruginosa, Stenotrophomonas maltophilia*, and *Staphylococcus aureus*. It also detects 21 antibiotic resistance genes such as the most common extended-spectrum beta-lactamases (ESBL), carbapenemases genes, and mecA gene.[22]

Multiplex PCR

Multiplex PCR is a flexible technique for enriching specific targets through amplification. It offers several advantages compared to whole genome and exome sequencing or hybrid capture methods, and is both cost-effective and time-efficient. It only requires a small amount of DNA (10–200 ng) as a starting material and works well even with low-quality DNA. Additionally, it provides comprehensive sequencing coverage and easy data analysis.

The effectiveness of PCR tests in molecular pathology has been well established, especially for identifying and amplifying targets from samples with limited DNA and low levels of targets. However, difficulties arise when scaling PCR primers and performing multiplex reactions. These difficulties include the creation of amplification errors from polymerase mistakes during the extension of oligomers and thermal damage to genomic targets, which can change the original nucleic acid sequence. In addition, reaction biases such as the formation of primer-dimers, competition for substrates, and sequence-based variations in PCR efficiency are common, particularly as the number of targets in a multiplex reaction increases.

Successful multiplex PCR relies heavily on well-designed primers. Important factors to consider during design include the length of the primer (18–25 nucleotides), consistency of melting temperature (within 1–2°C), optimal GC content (50–55%), and the need to avoid cross-complementarity. It is critical to steer clear of regions containing repetitive sequences or high homology, including known germ-line single nucleotide polymorphisms (SNPs), as these can influence PCR efficiency and lead to amplification bias. To ensure specificity to the target region and prevent unintentional amplification of pseudogenes or

similar regions, primers should be checked against SNP databases and sequence databases. Tools like Primer3 and PrimerBLAST are extremely useful for this aspect of primer design, helping to choose primers specific to the desired genomic sequences.

Multiplex PCR allows for the amplification of numerous short genomic sequences in a single reaction, which is especially useful when dealing with limited DNA quantities, such as those found in samples from small tumor biopsies or fine-needle aspirations. However, when working with small samples, the low DNA input can lead to biased amplification, potentially misrepresenting the cellular composition in the specimen. This issue can be addressed by using polymerases that have proofreading capabilities, although these enzymes typically have slower extension rates and lower thermostability.

Although there are difficulties, multiplex PCR offers benefits for sequencing DNA and RNA from samples of subpar quality, like formalin-fixed, paraffin-embedded (FFPE) tissue samples. The method's inclination towards amplifying short genomic regions (80–150 base pairs) supports successful sequencing, but if sequencing larger regions is needed, it may be necessary to split primer pairs into multiple pools or choose a capture-based method.

Like all amplification-based techniques, it is important to have strict procedures in place to avoid sample contamination. This involves keeping a physical barrier between the pre- and post-amplification areas, creating a workflow in one direction, and thoroughly decontaminating work surfaces. These steps are crucial to maintain the integrity of the amplification process and obtain precise sequencing outcomes.[23]

Multiplex PCR panels are an effective method for quickly identifying pathogens in patients with respiratory tract infections. Specifically, testing upper respiratory tract (URT) specimens with the BioFire Respiratory Panel 2 (BRP2), which primarily focuses on viruses,

reduces the time for pathogen identification, duration of antibiotic use, and hospital stay. Many clinical laboratories have validated the BRP2 for testing lower respiratory tract (LRT) specimens as well. The recently developed BioFire Pneumonia Panel (BPN) has demonstrated accurate identification of viruses and a wider range of bacteria in LRT specimens. Clinical laboratories now need to decide whether to include the BRP2, the BPN, or both in the test menu for LRT specimens, but there is currently no data comparing these assays in this particular context.[24]

FilmArray Pneumonia panel

The PN panel of FilmArray Pneumonia (PN panel; BioFire Diagnostics) is an innovative PCR-based tool for in vitro diagnostics, streamlining the process from sample to result. It is specifically designed to analyze native sputum (including endotracheal aspirates) and bronchoalveolar lavage (BAL) specimens, swiftly detecting bacteria, viruses, and genetic markers of antimicrobial resistance. What makes it unique is its efficiency, as it delivers comprehensive results in approximately 60 minutes with only about 2 minutes of hands-on time. The results of the PN panel are reported qualitatively, indicating whether a target is "detected" or "not detected" for viral and bacterial targets, including those associated with atypical pneumonia, as well as antibiotic resistance markers. In addition, it provides a semi-quantitative value for 15 other bacterial targets commonly found in respiratory infections. The speed, accuracy, and comprehensive analysis of this panel make it an invaluable tool for clinicians in rapidly diagnosing and managing pneumonia cases, enabling timely and targeted treatment interventions and improving patient outcomes.[25]

REVIEW OF STUDIES-

Jitmuang et al.[26] conducted a study from July 2019 to October 2021 assess the clinical usefulness of the BioFire FilmArray Pneumonia Panel Plus (BFPP) in the diagnosis of hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) in the presence of emerging antimicrobial resistance (AMR). Their findings were published in Frontiers in Cellular and Infection Microbiology in October 2022. The study aimed to evaluate how effective the BFPP is compared to standard microbiological tests and antimicrobial susceptibility testing (AST) in adult patients who were hospitalized. The results indicated that *A. baumannii, P. aeruginosa, and S. maltophilia* were the most commonly found organisms among the 40 subjects, most of whom were male, with a median duration of HAP/VAP diagnoses of 10.5 days. A significant proportion of Gram-negative bacteria demonstrated multidrug (MDR) or extensively drug-resistant (XDR) profiles. The BFPP successfully identified a diverse range of bacterial targets, with *A. baumannii, P. aeruginosa, and K. pneumoniae* being the most prevalent. Moreover, it frequently detected AMR gene targets such as CTX-M, OXA-48-like, and NDM. Comparative analysis revealed that BFPP exhibited excellent diagnostic sensitivity (98%) in identifying HAP/VAP aetiology, with a high negative predictive value (99%) but moderate specificity (81%) and positive predictive value (60%). However, limitations were observed, particularly the absence of *S. maltophilia* detection and discrepancies in AMR gene results, especially among *A. baumannii, P. aeruginosa*, and *S. aureus*. In conclusion, they emphasized the promising diagnostic performance of BFPP in identifying HAP/VAP pathogens, although with some limitations, underscoring the importance of continuous evaluation and improvement of diagnostic tools in the context of evolving antimicrobial resistance patterns.

Nathan Peiffer-Smadja et al [27] studied 85 HAP/VAP patients and collected BAL/PTC (plugged telescopic catheter) samples. They utilized the Unyvero hospitalised pneumonia test, a multiplex PCR that

can detect 21 bacteria and 19 resistance genes with a 5-hour turnaround time. They identified a total of 112 targets, out of which 90 were bacterial targets consisting of 5 CTX-M genes, 3 NDM, and 1 OXA-48 LIKE gene. Cultures showed *Legionella* growth in 2 patients. The multiplex PCR demonstrated a sensitivity of 80% and a specificity of 99%. Ensuring early effective treatment for 20 patients, early de-escalation for 37 patients, and avoiding unnecessary carbapenem use for 10 patients could reduce antibiotic resistance, broad-spectrum antibiotic usage, and mortality and morbidity related to severe pneumonia.

Lee et al. [28] conducted a research project to assess the efficiency of a multiplex PCR pneumonia panel in identifying respiratory pathogens and resistance markers in lower respiratory tract samples from adult ICU patients. The study compared the panel's performance with the standard test. Their results, published in the Journal of Microbiology, Immunology, and Infection, demonstrated that the FilmArray pneumonia panel effectively identified respiratory bacterial pathogens, with an overall positive agreement of 90% and a negative agreement of 97.4%. The panel also displayed potential in viral detection, identifying 16 viral targets compared to traditional methods. Coinfections were found in 42.3% of the samples. Despite differences in antimicrobial resistance gene detection, FilmArray PP was considered valuable, potentially influencing antibiotic prescriptions in 40.7% of patients. In summary, the research suggests that FilmArray PP provides a quick and sensitive diagnostic approach for lower respiratory tract infections, although clinical correlation is recommended to accurately interpret results, especially for multiple pathogens and antimicrobial resistance genes.

In 2016, **Chen et al.**[29] conducted a study analyzing the microbiome of sputum samples from 45 patients with community-acquired pneumonia. The results showed similarities at the phyla level compared to healthy controls, and stability at the genera level in *Streptococcus* spp. and

Neisseria spp. However, variations were observed in *Moraxella* spp. and *Rothia* spp. The study's findings suggested that *Rothia* spp. could potentially act as an endogenous pathogen in cases of pneumonia.

In 2015, **Wouter et al.** [30] conducted an important study which identified three separate microbiota profiles that were closely associated with pneumonia in elderly patients. These profiles included *Lactobacilli, S. pneumoniae*, and *Rothia* spp. The study suggested that pneumonia in these patients might be linked to an imbalance in the upper respiratory tract microbiome, characterized by an overgrowth of a single bacterial species along with specific anaerobic bacteria.

S Jain, et al. [31] The EPIC study, an extensive examination of pneumonia acquired in the community and affecting adults admitted to hospitals in the US, found significant differences in how often it occurred in various age groups. The rates of hospitalization due to pneumonia were notably higher in adults between 50 and 64 years old, 65 and 79 years old, and 80 or older, at about 4, 9, and 25 times respectively, compared to adults aged 18 to 49. Pathogens were found in 38% of cases, with viruses and bacteria identified in 27% and 14% respectively. The most commonly identified pathogens were *Human rhinovirus, Influenza virus*, and *S. pneumoniae*, with older adults experiencing the highest impact. The study reported an annual occurrence of 24.8 cases per 10,000 adults for community-acquired pneumonia requiring hospitalization, a figure similar to a study in Ohio conducted in 1991. However, differences in methodology, demographic changes, and healthcare delivery make direct comparisons between the two studies challenging. Variations in enrollment criteria, incidence estimations, and changes in demographics influenced the study's findings. Excluding recently hospitalized or severely immunocompromised patients and the more stringent use of radiographic confirmation in the case definition contributed to lower estimates compared to rates based on claims data.

D. M. Musher et al [32] conducted an observational study which tackled the issue of identifying the cause of community-acquired pneumonia. The researchers systematically applied approved diagnostic methods to patients who were hospitalized for pneumonia to determine the proportion in which an etiological agent could be identified. Out of the patients, 44 (17.0%) were found to be uninfected based on the final clinical diagnosis. Only 60 cases (23.2%) had a known causative bacterium. PCR found a respiratory virus in 42 cases (16.2%), with 12 of them also having a documented bacterial coinfection. Notably, in 119 cases (45.9%), no specific cause for pneumonia could be determined. Out of these cases, 69 (26.6%) displayed a syndrome indistinguishable from bacterial pneumonia. The study also delved into procalcitonin levels, showing elevated levels in patients with bacterial infections and low levels in uninfected individuals or those with viral infections. However, there was significant overlap in procalcitonin levels across the different groups.

N. J. Gadsby et al[33] conducted a study that addressed the challenge of diagnosing the cause of community-acquired pneumonia, which often makes it difficult to prescribe the right antimicrobial treatment. The study aimed to evaluate the effectiveness of a comprehensive test that detects multiple bacteria and viruses, including quantification, in adults who were hospitalized with pneumonia. The results showed that the comprehensive molecular testing of single lower respiratory tract specimens successfully identified pathogens in 87% of pneumonia patients, compared to the 39% detection rate achieved through traditional culture-based methods. The main pathogens identified were *Haemophilus influenzae* and *Streptococcus pneumoniae*, along with a variety of common and unusual pathogens. Viruses were found in 30% of cases, and 82% of these cases involved detection of both bacteria and viruses. A high percentage (85%) of patients had received antimicrobials in the 72 hours before being admitted to the hospital. Among these patients, PCR detected a bacterial pathogen in 78% of cases, whereas only 32% were found to be positive through culture

(P<.0001). The use of molecular testing showed potential benefits for antimicrobial management, as it made it possible to reduce the number and/or type of antimicrobials used in 77% of patients.

M. J. Loeffelholz et al,[34] and colleagues conducted a study comparing the effectiveness of diagnosing respiratory pathogens using the premarket version of the FilmArray Respiratory Panel (RP) multiplex PCR assay by Idaho Technology, Inc., with the FDA-cleared Prodesse ProFlu+, ProFAST+, ProParaflu+, Pro hMPV+, and ProAdeno+ real-time PCR assays by Gen-Probe. The study involved the analysis of 192 nasopharyngeal secretion specimens from 81 infants under the age of 1, all exhibiting upper respiratory tract symptoms. The FilmArray and Prodesse assays displayed significant overall agreement (94.3%) in cases where both commercial assays could detect common viruses, including adenovirus, human metapneumovirus, influenza A and B viruses, parainfluenza viruses 1 to 3, and respiratory syncytial virus. FilmArray PP detected a higher number of parainfluenza viruses compared to ProParaflu+, while ProAdeno+ identified more adenoviruses, although these differences were not statistically significant. FilmArray PP identified 138 additional pathogens not covered by the Prodesse assays, such as rhinovirus/humanenterovirus, bocavirus, coronavirus, and Mycoplasma pneumoniae. It is important to note that the FDA-cleared version of FilmArray PP, which was introduced after this study, includes targets such as *Adenovirus, Coronaviruses Hku1* and *NL63*, *Human metapneumovirus, Influenza A virus, Influenza A H1 seasonal virus, Influenza A H3 seasonal virus, Influenza A virus H1-2009, Influenza B virus, Parainfluenza viruses 1 To 4, Respiratory Syncytial Virus (RSV), Humanenterovirus/Rhinovirus*. The broader panel of the FilmArray PP assay allowed the identification of additional respiratory pathogens compared to the Prodesse assays, with *Rhinovirus* being the most prevalent additional pathogen in this group of young children with upper respiratory tract infection.

Kamel et al [35] conducted a study highlighting the importance of promptly identifying the microbial cause of pneumonia through diagnostic investigation. The main goal was to ensure that appropriate antibiotic treatment was administered in a timely manner and tailored to each individual patient. The researchers evaluated the FilmArray® Pneumonia Panel (FilmArray PP, BioFire Diagnostics), a multiplex PCR assay panel designed to detect 35 respiratory pathogens and resistance markers. Their research involved comparing its performance with the standard-of-care test in ICU patients with lower respiratory tract infections.

K H Rand et al [36] conducted a study that focused on the challenge of making decisions about antibiotic treatment for severely ill patients in the absence of microbiologic results. The study centered on the BioFire FilmArray Pneumonia Panel (PN), which has been recently cleared by the FDA. This panel uses multiplex PCR to semi-quantitatively detect 15 bacteria, 3 atypical pneumonia bacteria, 8 viruses, and 7 antimicrobial resistance markers in about 1 hour in the laboratory. Previous reports have indicated that the PN Panel is highly accurate in detecting bacteria, even in cases where routine culture did not yield any growth. The study involved testing bronchoalveolar lavage and endotracheal specimens submitted for culture from 270 patients between June and September 2018. Patients were divided into three groups: (1) those who tested positive in both culture and the PN Panel, (2) those who tested positive only in the PN Panel but had uninformative culture results (no growth or normal flora), and (3) patients with no PN Panel detections. The aim was to assess the PN Panel's performance compared to routine culture, especially in cases where culture results were inconclusive or unavailable.

Gilbert, James et al [37] While most observational studies find viral or bacterial pathogens in 50% or fewer patients admitted to the hospital with community-acquired pneumonia, they previously showed that the multi-test bundle (MTB) identified a potential pathogen in 73% of

patients. This research compares the detection rates for potential pathogens using the MTB versus the Biofire® Pneumonia FilmArray® panel (BPFA) multiplex PCR platform and outlines a method for integrating BPFA results to form the basis for subsequent antibiotic stewardship (AS) activities.

Kosai et al [38] carried out a study to evaluate the effectiveness of the BioFire FilmArray Pneumonia Panel (PN panel) for diagnosis. This automated and multiplexed nucleic acid detection system rapidly detects 26 pathogens, consisting of 18 bacteria and eight viruses, as well as seven antimicrobial resistance markers in a single test. Samples from the lower respiratory tract were tested using the PN panel, and the results were compared with those obtained from standard bacterial culture methods and antimicrobial susceptibility testing. Out of the 57 samples analyzed, the PN panel successfully identified 97 targets, including 84 bacteria, four viruses, and nine antimicrobial resistance markers. Importantly, the PN panel demonstrated a threefold higher detection rate for bacteria and antimicrobial resistance compared to bacterial culture methods, which only identified 25 bacteria and two resistant isolates relevant to the panel's targets. The overall positive and negative percentage agreements between the PN panel and culture methods for bacterial detection were 100.0% and 92.9%, respectively. The PN panel detected the presence of multiple pathogens in 42.1% of the samples, with the number of pathogens ranging from two in 19.3% of the samples to six in 1.8% of the samples. The semi-quantitative analysis by the PN panel indicated higher copy numbers (≥ 10^6 copies/mL) of bacterial targets when bacteria were confirmed by the culture method. Conversely, variable semiquantitative values (10^4 to 10^7 copies/mL) were observed among bacteria that were not detected by the culture method.

Gabriel Cojuc-Konigsberg et al[39] The findings from this research aligned with a prior prospective cohort study carried out in a

specialized medical facility in Mexico City that was transformed into a COVID-19 hospital. In COVID-19 patients with VAP, enterobacteria were the most commonly identified microbial isolate, followed by non-fermenting Gram-negative bacilli and cases of polymicrobial infections. Additionally, this study observed antimicrobial resistance in approximately 50% of VAP cases, primarily due to beta-lactamases, specifically AmpC producers.

Michael S. Niederman et al [40] conducted a study in USA, focused on severe community-acquired pneumonia, which is associated with high morbidity and mortality, requiring ICU care, mechanical ventilation, and inotropic support. The PSI-Pneumonia severity index is utilized as a prognostic score. ICU care was necessary for 23% of patients, 20% received non-invasive ventilation, and 24% required mechanical ventilation. The primary causative organism was *Strep pneumoniae*, while others included *MRSA, P. aeruginosa*, and various gram-negative bacteria, along with emerging viral pathogens. Additionally, *Legionella* was frequently associated with the condition.

MATERIALS AND METHODS

- Clinical Specimens. ET secretions, BAL, and sputum were taken from hospitalized patients at DMCH Ludhiana.
- Multiplex Real-Time PCR Assay. The specimens collected from ET secretions, BAL, and sputum underwent analysis using a multiplex PCR pneumonia panel.
- Standard Methods. Sputum, ET, BAL samples were subjected to gram stain and culture sensitivity testing.

Source of Data:

Hospitalized patient populations who had clinical features of pneumonia and X-ray changes.

METHOD OF COLLECTION OF DATA

Inclusion Criterion:

Include:

- Hospitalized patients
- In-patient in ward/ICU/CCU
- Breathing spontaneously or intubated
- About to receive antibiotics for LRTI on admission
- Have cardinal signs of pneumonia(new lung infiltrate, lobar consolidation, cavitation on chest xray, clinical evidence{fever, dyspnea, cough and sputum production})

Exclusion Criterion

Includes:

- All outpatients
- Not consenting for study
- Already started on antibiotics before admission in DMCH

DURATION OF STUDY/ NUMBER OF CASES

15th September 2022 to 15th September 2023

OUTCOME

To compared the differences in diagnosis, clinical cure, and antimicrobial selection between patients treated according to FilmArray results and those treated with standard methods.

STATISTICAL ANALYSIS:

Data was described in terms of range, mean ± standard deviation (± SD), median, frequencies (number of cases), and relative frequencies (percentages) as appropriate. To determine whether the data was normally distributed, a Kolmogorov-Smirnov test was used. For comparing categorical data, a Chi-square ($\chi 2$) test was performed, and a Fisher exact test was used when the expected frequency was less than 5. The numbers of true-positive (TP), true-negative (TN), false-positive (FP), and false-negative (FN) results were calculated. A probability value (p-value) less than 0.05 was considered statistically significant. All statistical calculations were done using the Statistical Package for the Social Sciences (SPSS) version 21 (SPSS Inc., Chicago, IL, USA) for Microsoft Windows in the cross-sectional study analysis.

OBSERVATIONS & RESULTS

Table 1: Patient Demographics Summary

Age Interval	Number of Patients	percentage
18-20	2	2.41%
20-29	14	16.87%
30-39	8	9.64%
40-49	13	15.66%
50-59	18	21.69%
60-69	17	20.48%
70-79	6	7.23%
80-89	5	6.02%
Total	83	100%

The patient demographics summary reveals a diverse distribution across age groups. The majority of patients fall between 50 and 69 years old, constituting 42.17% of the total population, with the highest representation in the 50-59 age bracket (21.69%). Patients under 20 and those aged 80-89 each comprise the smallest proportions at 2.41% and 6.02%, respectively. This data underscores the importance of age considerations in healthcare management and resource allocation within the given population.

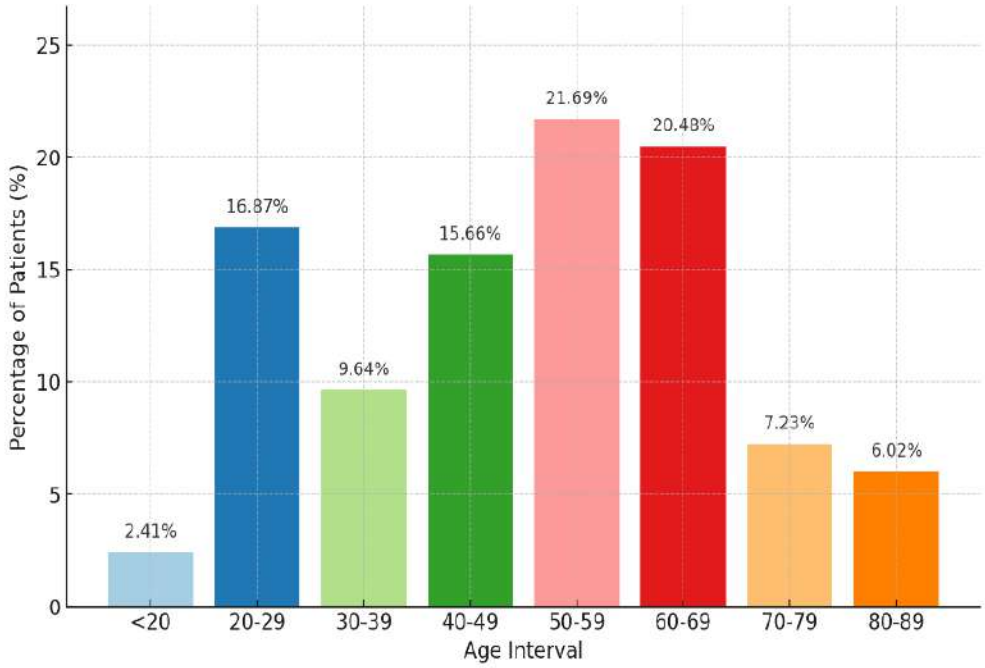

Figure 1: Patient Demographics Summary: Age Distribution

Table 2: Gender Distribution

Gender	Number of Patients	percentage
Male	52	62.6%
Female	31	37.4%

The table presents the gender distribution among patients, with 52 males and 31 females. This data provides insight into the demographic composition of the patient population, indicating a higher representation of males compared to females. Understanding such gender disparities can be crucial for healthcare providers in tailoring treatments and interventions to address the specific needs and health concerns of different gender groups effectively.

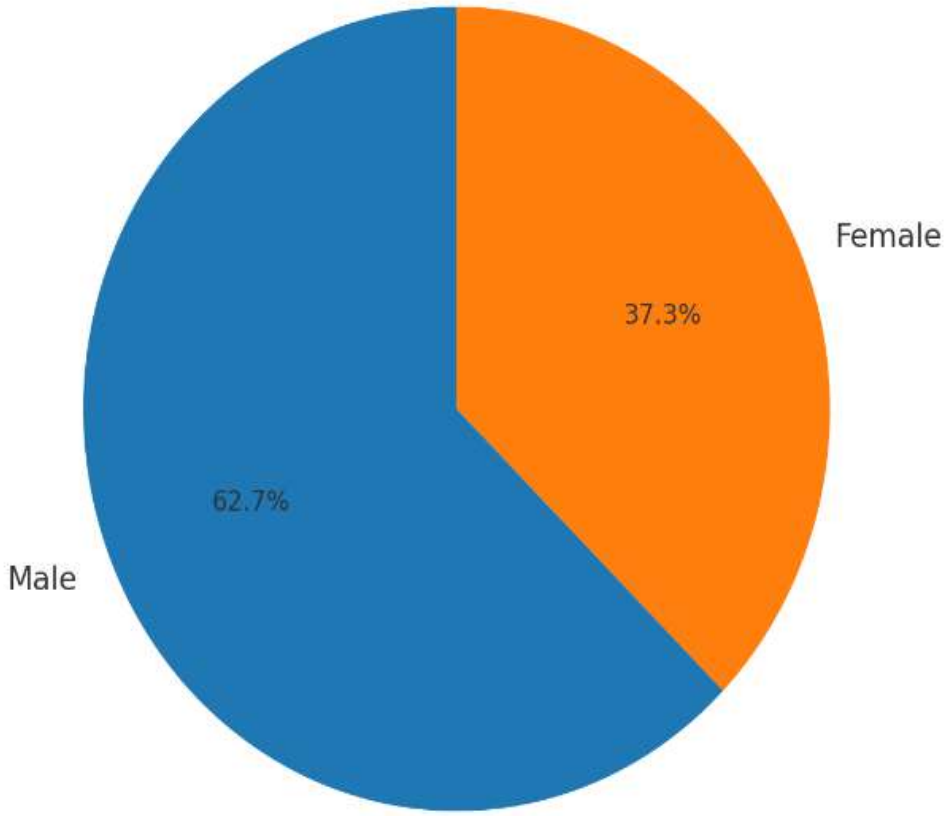

Figure 2: Gender Distribution

Table 3: Distribution of study participants according to complaints

Complaint	Number of Patients	percentage
Fever	61	35.06%
Dyspnea/SOB	65	37.36%
Cough	43	24.71%
Chest Pain	3	1.72%
Others	2	3.14%

The table illustrates the distribution of complaints among patients, revealing that dyspnea or shortness of breath is the most prevalent, reported by 65 patients, constituting 37.36% of the total complaints. Fever follows closely behind, affecting 61 patients (35.06%). Cough is also a common complaint, with 43 patients (24.71%) experiencing it. Chest pain seen in 3 patients (1.72%). Least common was pedal edema, and altered sensorium, each affecting only a small percentage of patients. This breakdown provides valuable insights into the primary concerns and symptoms presenting in the patient population.

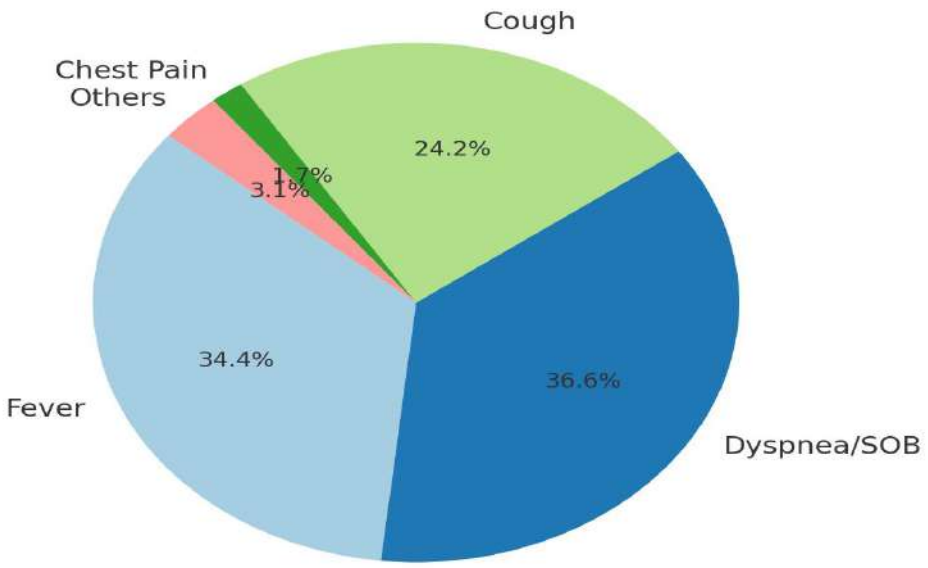

Figure 3: Distribution of study participants according to complaints

Table 4: Distribution of study participants according to Co-morbidities

Comorbidity	Number of Patients	percentage
Diabetes/DM	36	43.3%
Hypertension/HTN	31	37.3%
COPD	5	6.02%
CAD	11	13.2%
ILD/SARCOIDOSIS	2	2.4%
OTHERS	30	38.5%
NO COMORBIDITY	20	24.09%

The table presents comorbidities among patients, revealing that diabetes (DM) and hypertension (HTN) are prevalent, affecting 26.67% and 22.96% of patients, respectively. Chronic obstructive pulmonary disease (COPD) is present in 3.70% of cases. Coronary Artery Disease (CAD) seen in 11 patients (13.2%). Least common was Interstitial Lung Disease (ILD) in 2 patients (2.4%). The category "OTHERS" encompasses a majority of comorbidities, representing 38.5% of patients, and 24.09% patients had no underlying comorbidity, highlighting the diverse health conditions complicating the patient population.

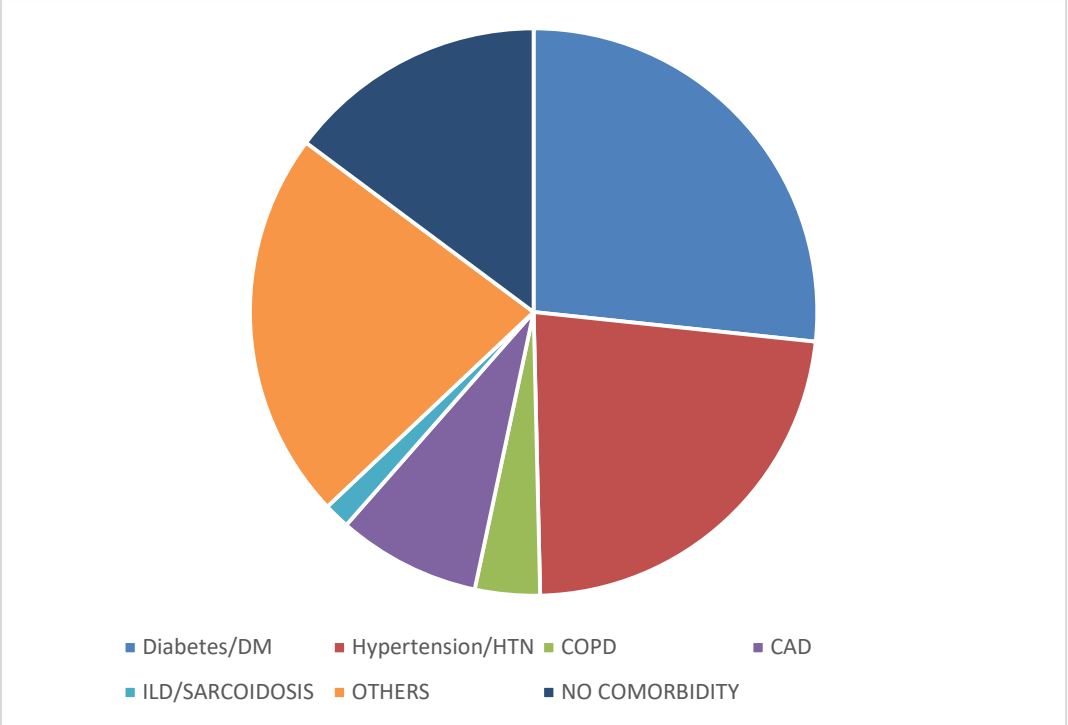

Figure 4: Distribution of study participants according to Co-morbidities

Table 5: Oxygen Saturation at Room air on presentation

Saturation Range	Number of Patients	percentage
100-96%	6	7.20%
95-91%	6	7.20%
86-90%	22	26.50%
85-81%	18	21.60%
80-76%	11	13.20%
75-71%	6	7.20%
<70%	6	7.20%
Gasping	8	9.60%

The table presents the oxygen saturation levels of patients upon admission, categorizing them into various ranges. Among the patients 7.20% were in 100-96% and 95-91% saturation on room air categories each. Large number of patients 22 (26.50%) falls in range of 85-81% saturation on room air when presented initially. 18 patients (21.60%) had saturation of 80-76% on room air on presentation. Fewer patients 6 (7.20%) were in 71-75% and <70% saturation category each. Few (9.60%) presented in gasping state. This data underscores the importance of monitoring oxygen saturation upon admission and tailoring interventions accordingly to ensure optimal patient care.

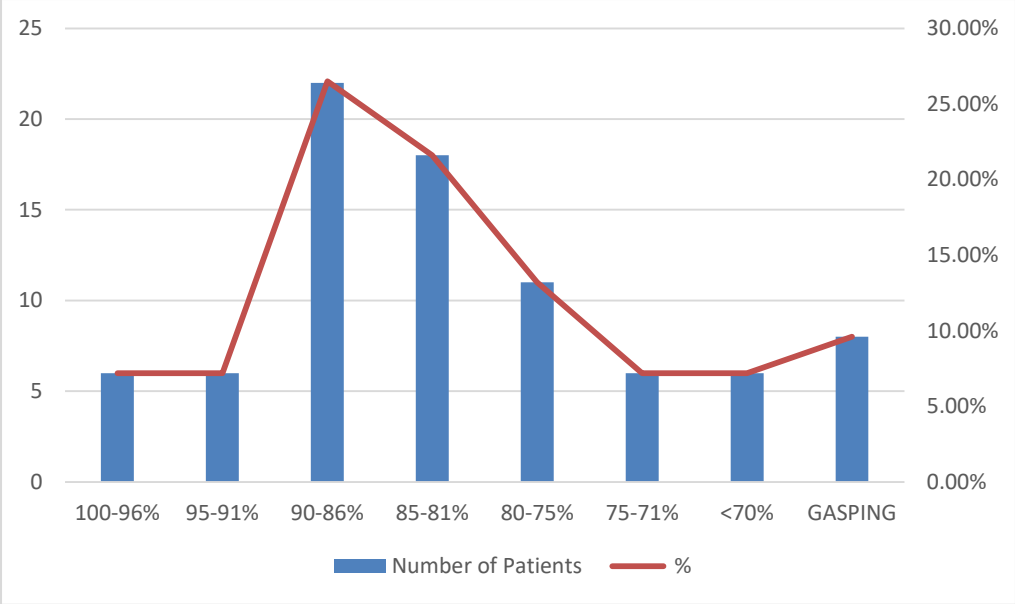

Figure 5: Oxygen Saturation at Room air on presentation

Table 6: Auscultation Findings

Finding	Number of Patients	percentage
Crepitations	42	50.60%
Rhonchi	8	9.60%
Both crepitations and rhonchi	4	4.81%
NVBS	11	13.2%
Other	18	21.68%

The table presents the auscultation findings of patients, revealing various respiratory sounds encountered during examination. Among the observed findings, crepitations were the most prevalent, identified in 42 cases, constituting 50.60% of the total. Rhonchi were noted in 8 patients, accounting for 9.60%, while Normal vesicular breath sounds (NVBS) were observed in 11 cases, making up 13.2%. The remaining encompassed 4 patients with both crepitations and rhonchi, and other respiratory sounds like decreased breath sounds detected during auscultation in 18 patients (21.68%), highlighting the diverse range of conditions encountered in clinical practice.

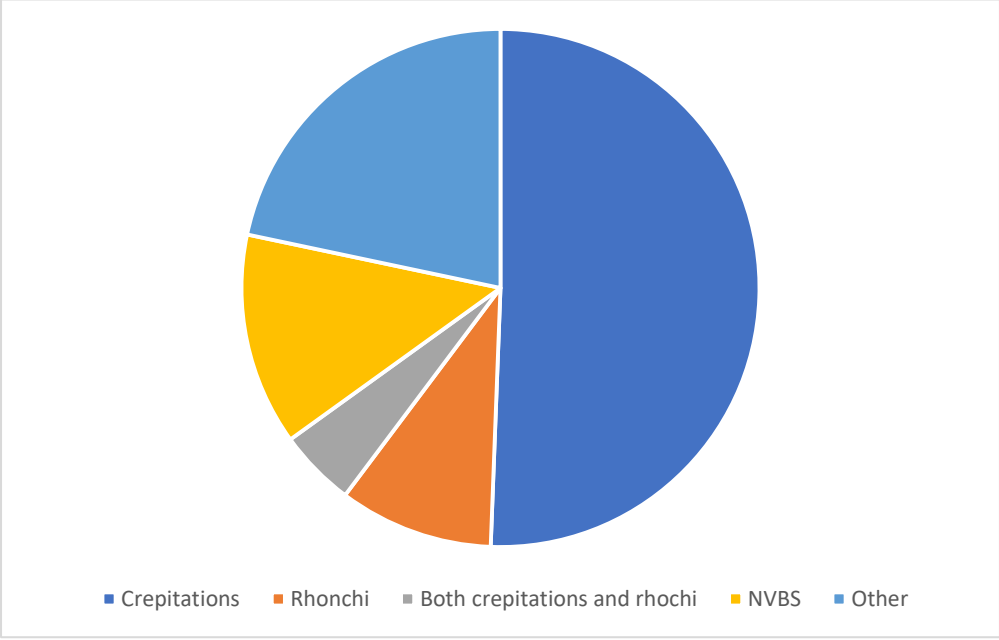

Figure 6: Auscultation Findings

Table 7: CXR Findings

Finding	Number of Patients	percentage
Consolidation	28	33.73%
ARDS	6	7.22%
Haziness	12	14.45%
Effusion	21	25.30%
Opacities	4	4.81%
Clear	2	2.40
Others	10	12.04%

The table summarizes the chest X-ray (CXR) findings from a group of patients, indicating a diverse range of pulmonary conditions. Consolidation is the most prevalent finding, observed in 33.73% of cases, followed by pleural effusion (25.30%) and then haziness (11.34%). ARDS is present in 7.22% of patients, while opacities are relatively rare, occurring in only 4.81% of cases. 2 patients had clear chest X-ray. Only 10 patients had varied pulmonary abnormalities like lung collapse, surgical emphysema etc. These findings underscore the complexity and heterogeneity of respiratory conditions diagnosed through CXR examinations in this patient population.

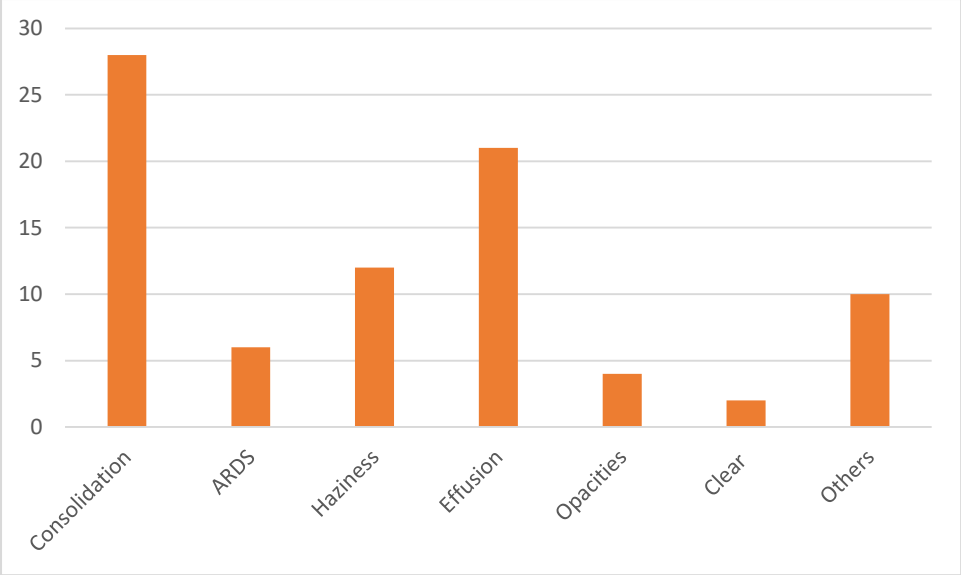

Figure 7: CXR Findings

Table 8: DAYS OF ADMISSION AFTER WHICH FILM ARRAY WAS DONE

DAYS	NO OF PATIENTS	PERCENTAGE
SAME DAY	4	4.8%
1-3 DAYS	37	44.5%
4-7 DAYS	24	28.9%
>7 DAYS	18	21.6%

This table illustrates the days of admission after which film array was done. Only few patients 4.8% had film array done on the day of admission. Majority, 37 patients (44.5%) lies in the group of day 1-3 days of admission. In 24 patients (28.9%), film array was done in 4-7 days after admission. Also 18 patients (21.6%) had their film array done after a week of admission. The heterogenicity of this table implies the individual nature of clinical practices.

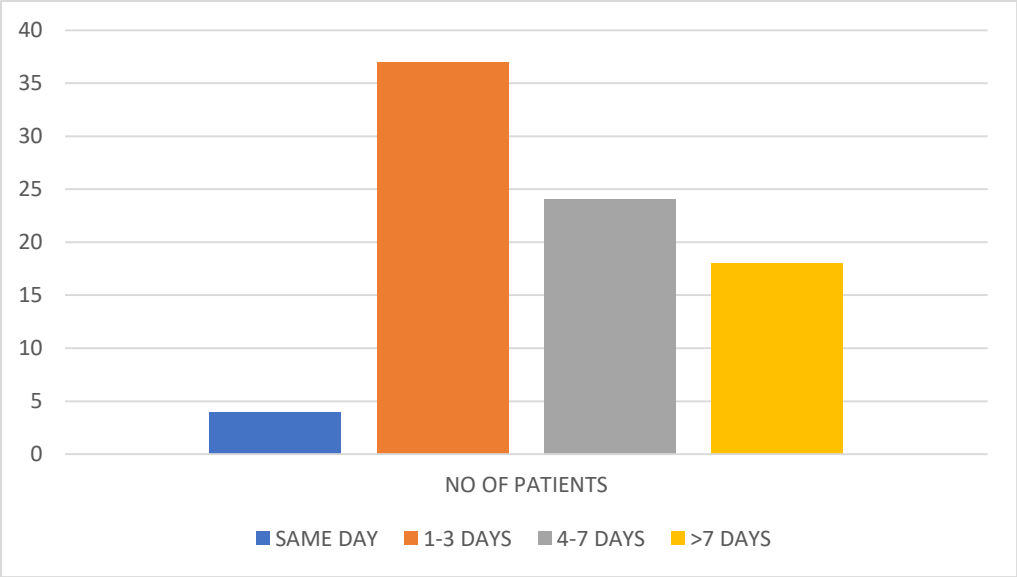

Figure 8: DAYS OF ADMISSION AFTER WHICH FILM ARRAY WAS DONE

Table 9. SAMPLE USED FOR TESTING

Sample Type	Number of Patients	Percentage
Sputum	31	37.35%
BAL	3	3.61%
ET SECRETION	49	59.04%

The table presents the distribution of sample types used for testing, with sputum constituting 37.35%, bronchoalveolar lavage (BAL) 3.61%, and endotracheal secretion (ET secretion) 59.04% of the total samples. Notably, the majority of samples are ET secretions, indicating a signifying the majority of patients were intubated during hospital stay.

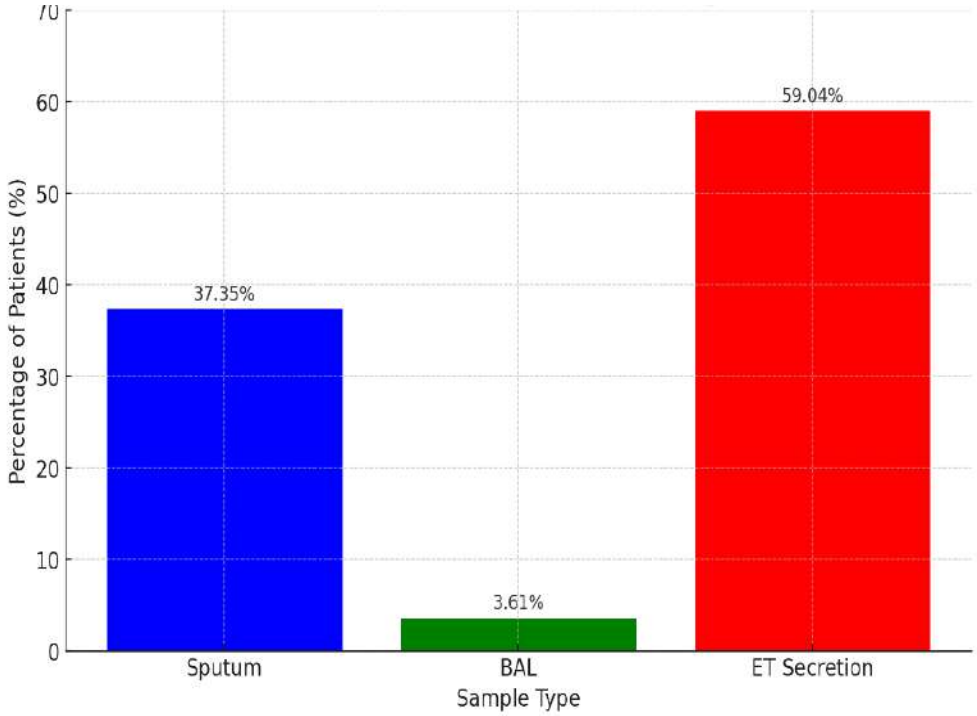

Figure 9. SAMPLE USED FOR TESTING

Table 10: No. of targets detected on FilmArray

Targets	No of patients	percentage
Single bacteria	14	16.8%
>1 bacteria	16	19.2%
Single virus	16	19.2%
>1 virus	2	2.4%
Both bacteria and virus	28	33.7%
No organism found	7	8.4%

In this table, we found out that 28 patients had co-existing both bacteria and virus in the same person. Single bacteria were found in 14 patients whereas single virus was found in 16 patients. 16 patients had >1 bacterial targets in their film array report. Only 2 patients had multiple viruses. 7 patients had no targets found in their film array report.

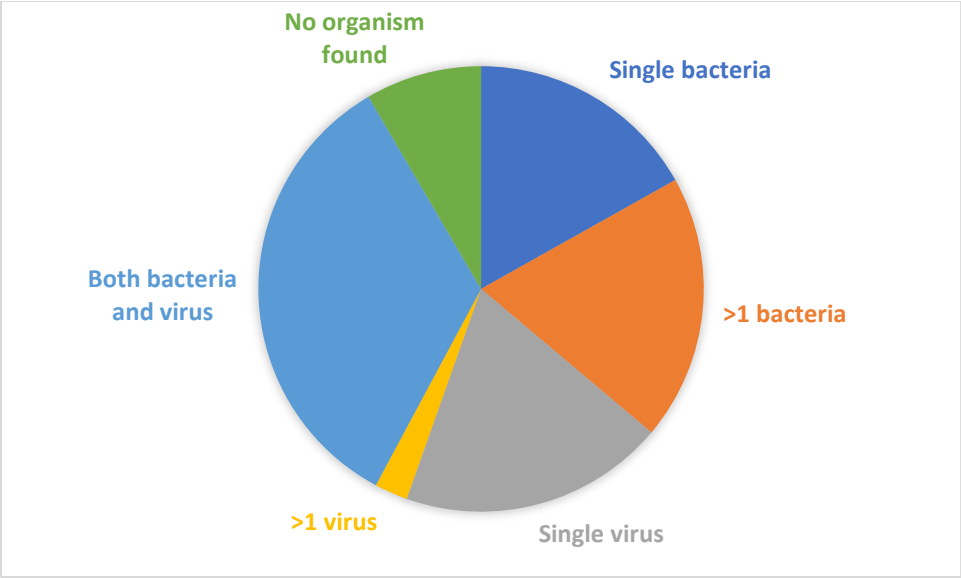

Figure 10: No. of targets detected on FilmArray

Table 11. Distribution of Bacterial targets on Film Array

Bacteria (n=116)	Number of targets	Percentage
Acinetobacter baumannii	28	24.13%
Haemophilus influenzae	8	6.8%
Klebsiella pneumoniae	27	23.2%
Staphylococcus aureus	13	11.2%
Pseudomonas aeruginosa	12	10.34%
Escherichia coli	13	11.%
Enterobacter cloacae	5	4.31%
Streptococcus agalactiae	5	4.31%
Streptococcus pneumoniae	3	2.5%
Serratia marcescens	1	0.8%
Proteus mirabilis	1	0.8%

The above table illustrates the results from the FilmArray test, which identifies a variety of pathogens in patients. *Acinetobacter baumannii* is the most frequently detected organism, representing 24.13% of bacterial targets, *K. pneumoniae* 27 (23.2%) followed by *Staphylococcus aureus* and *E. coli* is found in 13 patients each, making up 11.2%, followed by *Pseudomonas aeruginosa* making 10.34% and then *H.influenzae* comprising 6.8% of total bacterial targets. *Enterobacter cloacae* and *Streptococcus agalactiae* making 4.3%, *Streptococuss pneumoniae* 2.5% and *Serratia* and *Proteus mirabilis* both having lowest percentage of all the bacterial targets.

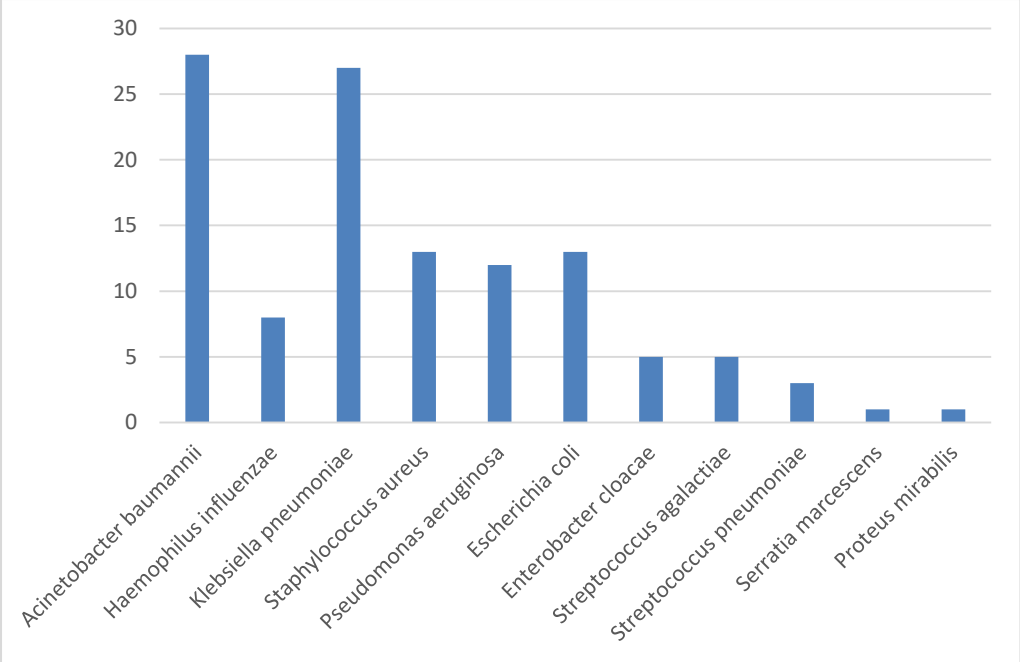

Figure 11: Distribution of Bacterial targets on Film Array

Table 12: Distribution of viral targets on film array

Virus(n=49)	No of targets	percentage
Influenzae A	14	28.5%
Influenzae B	9	18.3%
Humanenterovirus/Rhinovirus	8	16.3%
Coronavirus	4	8%
RSV	4	8%
Adenovirus	5	10%
Parainfluenzae virus	3	6%
H1N1	1	2%
Metapneumovirus	1	2%

In above table, *Influenzae A* was detected in 14 samples followed by Influenzae B which was seen in 9 samples (18.3%) and *Humanenterovirus/rhinovirus* which was found in 8 samples (16.3%). *Adenovirus* seen in 10% of total viral targets. *Coronavirus* and RSV were found in 8% followed by *Parainfluenzae virus* which was seen in 6% and H1N1 and *Metapneumnovirus* making only 2% of total viral targets. The detection of viruses was seen only in film array and no virus was cultivable in culture method.

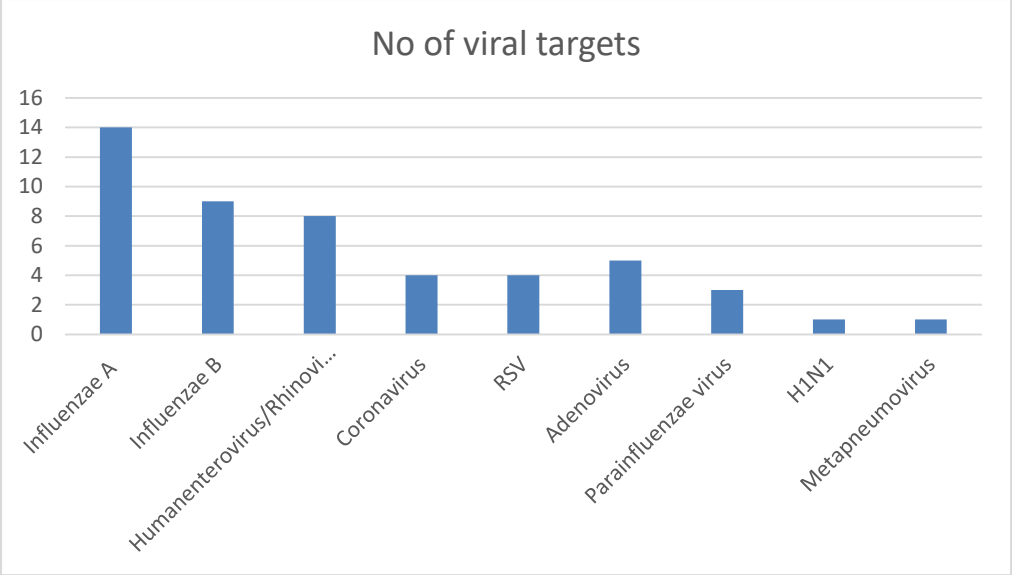

Figure 12: Distribution of viral targets on film array

Table 13. Gram Stain Results

Result	Number of Patients	Percentage
Micro-organism not found	26	31.33%
Micro-organism found	57	68.67%

The Gram Stain Results table summarizes findings from a patient cohort, revealing that 26 patients (31.33%) no micro-organism was found, while the remaining 57 patients (68.67%) showed presence of various micro-organisms. This data suggests a significant portion of patients may have presence of micro-organisms in gram stain warranting further investigation or treatment.

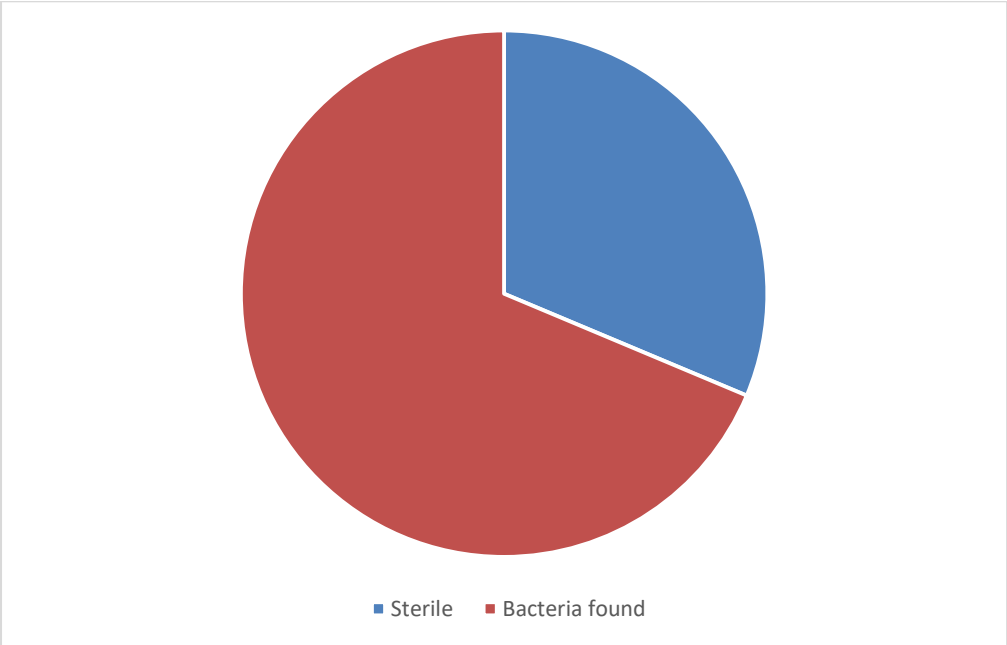

Figure 13: Gram Stain Results

Table 14: Targets detected on culture media

Result	Number of Patients
Acinetobacter baumannii	15
Klebsiella pneumoniae	12
Escherichia coli	2
Pseudomonas aeruginosa	3
Enterobacter cloacae	1
Staphylococcus hominis	2
Citrobacter koseri	1
Stenotrophomonas maltophilia	1
No growth	53

The culture results indicate that among the patients tested, 53 cultures showed no growth, while 15 patients had *Acinetobacter baumannii*, 12 cultures showed *Klebsiella pneumoniae*. *Pseudomonas* seen in 3 cultures, *Escherichia coli* seen in 2 patients and *Enterobacter cloaca, Staphylococcus hominis, Citrobacter koseri* and *Stenotrophomonas* showed growth in one patient each. This data underscores the prevalence of negative cultures among the patients, suggesting potential implications for treatment strategies and healthcare management.

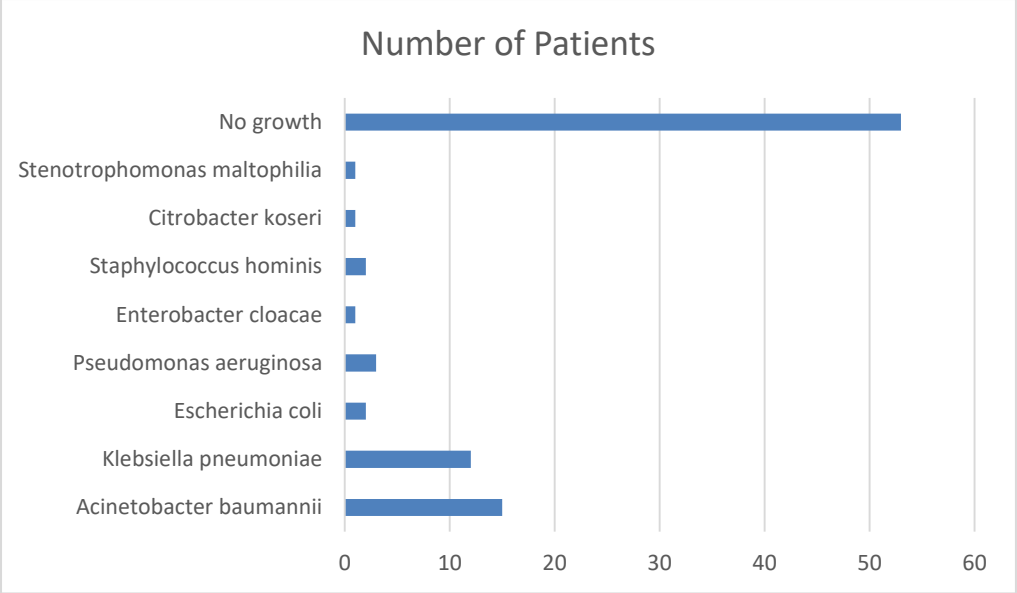

Figure 14: Targets detected on culture media

Table 15: ORGANISMS DETECTED IN CULTURES AND FILM ARRAY

ORGANISM DETECTED	CS+PP+	CS+PP-	CS+PP-	CS-PP+	PPV	NPV	Sn	Sp
ACINETOBACTER BAUMANNII	14	1	14	54	50%	100%	93%	79%
K. PNEUMONIAE	8	4	19	52	30%	90%	66%	73%
E. COLI	1	2	12	68	100%	100%	33%	85%
P. AERUGINOSA	2	0	10	71	20%	100%	100 %	87.7%
H. INFLUENZAE	0	0	8	75	0%	100%	NA	90%
STAPH AUREUS	0	0	13	70	0%	100%	NA	84%
STREP PNEUMONIAE	0	0	3	80	0%	100%	NA	96%
ENTERBACTER CLOACAE	0	0	5	78	0%	100%	NA	94%
STREP AGALACTIAE	0	0	5	78	0%	100%	NA	94%
TOTAL FOR BACTERIA	25	7	89	626	20%	100%	78.1 %	87.6%

Here=PPV=Positive predictive value, NPV=negative predictive value, Sn=sensitivity, Sp=specificity

This table illustrates the comparison between yield of pneumonia panel and culture growth report. Bacterial targets were detected majority times on pneumonia panel as compared to culture growth, in 8 patients *Acinetobacter* were found in both culture growth and pneumonia panel, in 1 patient it was positive only in culture growth and not on pneumonia panel and in 14 patients it was found only on pneumonia panel and was not found on culture growth with a PPV OF 50% and NPV of 100%. *Klebsiella pneumoniae*- in 8 patients the organism was found in both culture and pneumonia panel, in 4 patients only on culture method and in 19 patients on pneumonia panel with sensitivity of 66% and specificity of 73%. *Staph aureus* was seen in film array in 13 patients with NPV of 100% and specificity of 84%. FA is 87.6% specific and 78.1% sensitive for bacteria. It 20% PPV and100% NPV for bacteria. All the virus detected were not found in any culture growth but only found in the pneumonia panel thus implying the high diagnostic accuracy of this method.

Table 16: Quantitative assessment of organisms detected in culture and pneumonia panel

Pneumonia panel (copies/ml)	**Culture (CFU/ml) not detected**	**$<10^3$**	**10^4**	**$>10^5$**
Not detected	0	7	1	2
10^4	39	1	2	1
10^5	17	3	0	1
10^6	10	0	1	1
$>10^7$	30	6	3	6

In the above table, 96 organisms were found to be detected on pneumonia panel in various samples when compared to standard methods and only 10 organisms were seen in culture method in various samples which were not seen on pneumonia panel. Various organisms which low CFU/ml in culture growth, were detected in high copies/ml in pneumonia panel. Organisms with copy number $<10^3$ were not detected on film array. This shows the qualitative superiority of pneumonia panel as compared to standard culture in detecting target organisms.

Table 17. Resistance Gene Detection

Gene Detected	Number of samples	%
Present	49	59.04%
Absent	34	40.96%

The table depicts the findings of resistance gene detection in a patient cohort. Among the individuals analyzed, 49 samples (59.04%) were found to have the resistance gene present, while 34 samples (40.96%) showed its absence. This data suggests a substantial prevalence of the resistance gene within the studied population, potentially impacting treatment strategies and highlighting the significance of targeted interventions in managing resistant strains.

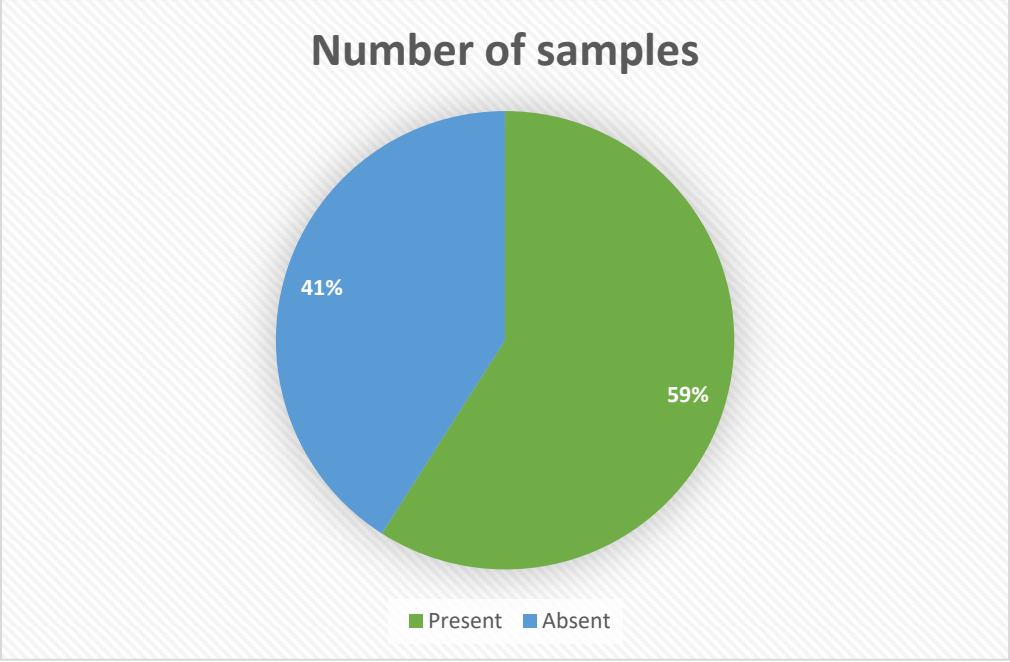

Figure 15. Resistance Gene Detection

Table 18: Distribution of resistance genes according to bacterial targets

ORGANISM	KPC	CTX-M	IMP	VIM	OXA-48 LIKE	NMD	TOTAL
A.baumannii	0	19	3	11	15	26	74
K.pneumoniae	1	23	6	13	27	27	97
E.coli	1	11	3	7	10	12	44
Enetrobacter cloacae	0	2	2	4	3	4	15
P.aeruginosa	0	6	4	5	6	11	32
Total	2	61	18	40	61	80	262
Percentage	0.7%	23.2%	6.8%	15.2%	23.2%	30.5%	100%

We analysed resistance gene distribution according to the bacterial target and found that majority 80 (30.5%) targets out of 262 were having NDM gene followed by CTX-M and OXA-48 LIKE in 61 bacterial targets (23.2%). 40 bacterial targets were having resistance gene VIM. 18 targets showed presence of IMP and only 2 had the presence of KPC gene which were not seen on culture media due to empirical antibiotics given before sending culture media.

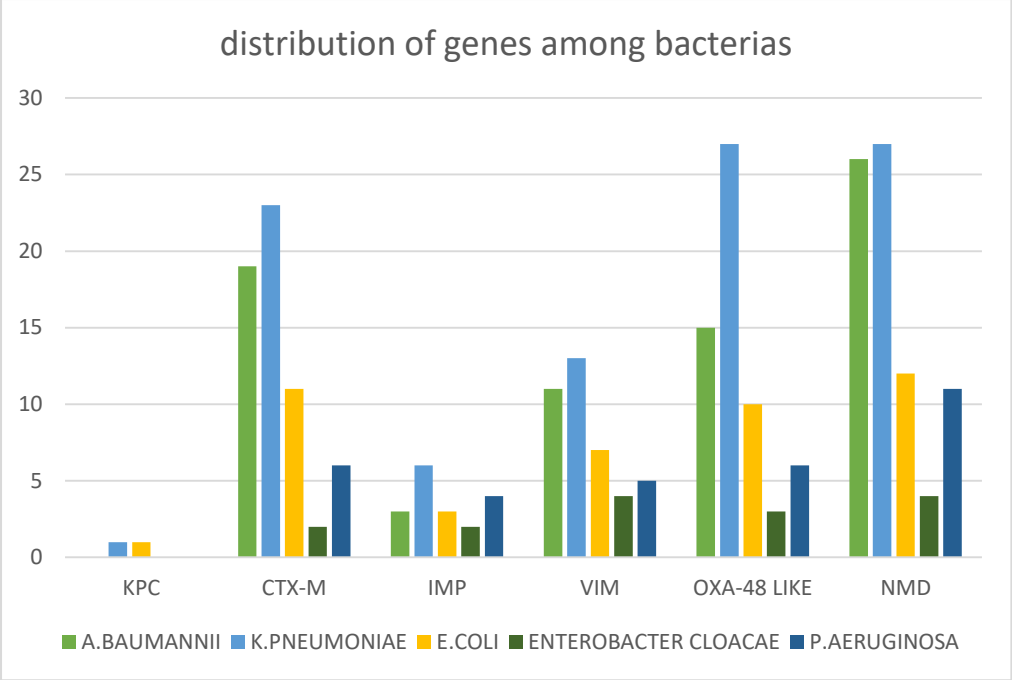

Figure 16: Distribution of resistance genes according to bacterial targets

Table 19. Empirical Antibiotic Treatment

Antibiotic	Number of Patients	Percentage
MEROPENEM, TEICOPLANIN	47	56.63%
MEROPENEM, TEICOPLANIN, AZITHROMYCIN	19	22.89%
PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN	10	12.05%
Others	7	8.43%

The table presents data on empirical antibiotic treatment utilized for patients, showcasing the frequency of different antibiotic combinations. Meropenem paired with teicoplanin emerged as the predominant choice, constituting 56.63% of cases, followed by a combination of meropenem, teicoplanin, and azithromycin at 22.89%. A smaller proportion received a regimen of piperacillin, tazobactam, and azithromycin, comprising 12.05% of cases, while the remaining 8.43% received other antibiotic combinations. This breakdown offers insight into prevailing empirical treatment strategies for patients, highlighting the predominant use of meropenem and teicoplanin in various combinations.

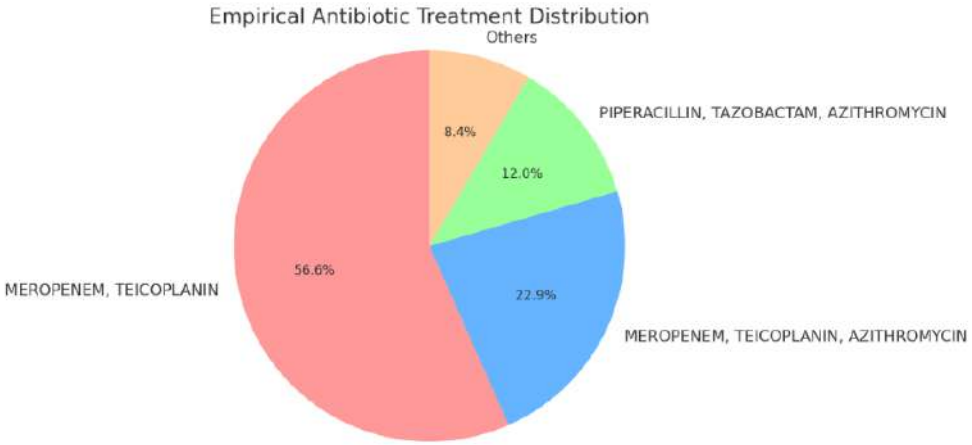

Figure 17. Empirical Antibiotic Treatment

TABLE 20: COMPARISON OF PNEUMONIA PANEL AND CULTURE METHOD IN ANTIBIOTIC SENSITIVITY AND RESISTANCE

TARGET ON PENUMONIA PANEL & CULTURE METHOD	RESISTANCE GENE	CULTURE SENSTIVITY
ACINETOBACTER BAUMANNII	NDM, CTX-M, OXA-48 LIKE	COLISTIN
ACINETOBACTER BAUMANNII	NDM, CTX-M, VIM	COLISTIN, AMIKACIN, MINOCYCLINE
ACINETOBACTER BAUMANNII	NDM	COLISTIN
ACINETOBACTER BAUMANNII	NDM, CTX-M, OXA-48 LIKE, VIM	COLISTIN, MINOCYCLINE
E. COLI	CTX-M, NDM, VIM, OXA-48 LIKE	COLISTIN, AMIKACIN, GENTAMICIN, TIGECYCLINE
K. PNEUMONIAE	IMP, NDM, CTX-M, OXA-48 LIKE, VIM	COLISTIN, AMIKACIN, GENTAMICIN
K. PNEUMONIAE	NDM, CTX-M, OXA-48 LIKE	COLISTIN, AMIKACIN, TIGECYCLINE
K. PNEUMONIAE	IMP, NDM, VIM, OXA-48LIKE	COLISTIN, TIGECYCLINE, TETRACYCLINE, DOXYCYCLINE
PSEUDOMONAS AERUGINOSA	NDM, VIM, IMP	COLISTIN
PSEUDOMONAS AERUGINOSA	NDM, CTX-M	COLISTIN

This table describes the presence of resistance gene on film array and sensitivity pattern on culture method. Eg *Acinetobacter baumannii* had carbapenemase resistance, extended spectrum resistance, showed sensitivity only to colistin when culture methods were obtained. *E. coli* when detected with beta lactamase, carbapenemase, extended spectrum resistance showed sensitivity to fewer aminoglycosides and polymyxin. *K. pneumoniae* similarly showed extended spectrum resistance genes had sensitivity to fewer aminoglycosides, polymyxin only.

Table 21. Antibiotics Revised After FilmArray Report

Antibiotic Change	Number of Patients	Percentage
NOT CHANGED	20	24.10%
CHANGED	63	75.9%

Following a comprehensive analysis of patient data utilizing the FilmArray system, revisions in antibiotic prescriptions were implemented. Among the alterations, 24.10% of patients saw no changes in their antibiotic regimen. Majority patients 63 (75.9%) had change in antibiotic regimen after film array report. This signifies the importance of film array in antibiotic stewardship.

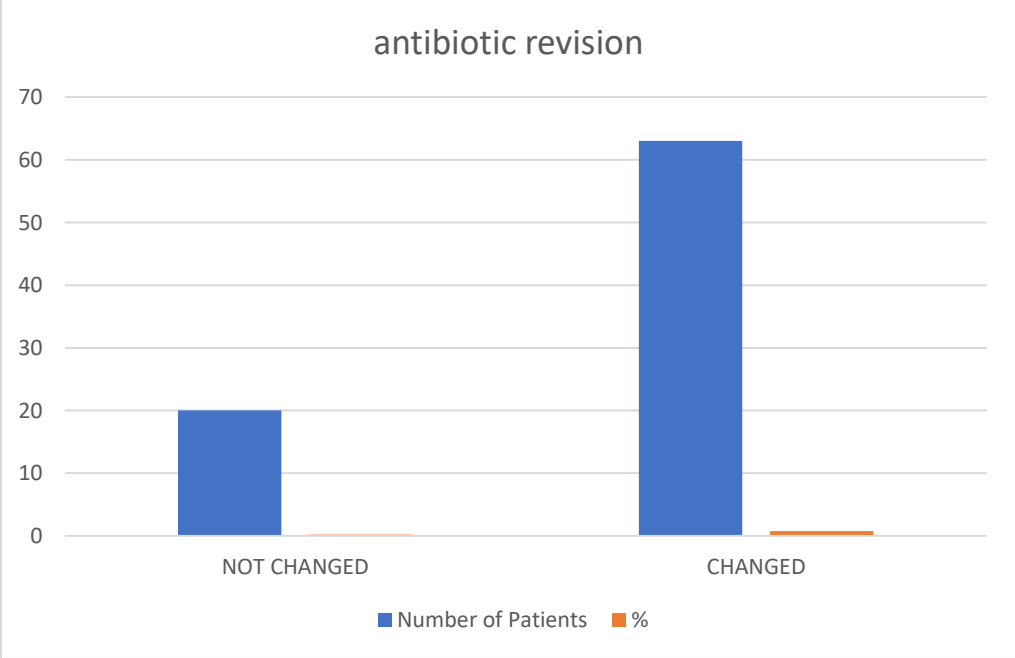

Figure 18. Antibiotics Revised After FilmArray Report

Table 22: Duration before Changing Antibiotics after FilmArray Test.

Days after test	Number of Patients	Percentage
0-1 Days	14	16.8%
2-3 Days	10	12.04%
4-5 Days	9	10.84%
More than 5 Days	30	36.14%
Not Changed	20	24.10%

The above table illustrates the duration before changing antibiotics after the FilmArray test. Among the patients, 16.8% had their antibiotics changed within 0-1 days after receiving the test results, indicating an immediate response to the diagnostic information provided. A smaller proportion, 12.04%, experienced changes in their antibiotic regimen within 2-3 days, and an equal percentage saw changes occur within 4-5 days. Notably, 36.14% of patients had their antibiotics adjusted more than five days after the test, suggesting a delayed response in some cases. Meanwhile, 24.10% of patients did not have any changes made to their antibiotic treatment, highlighting scenarios where the initial treatment was maintained despite the new diagnostic data. This distribution underscores the variability in clinical response times following FilmArray testing and emphasizes the importance of timely diagnostic information in guiding effective antibiotic therapy.

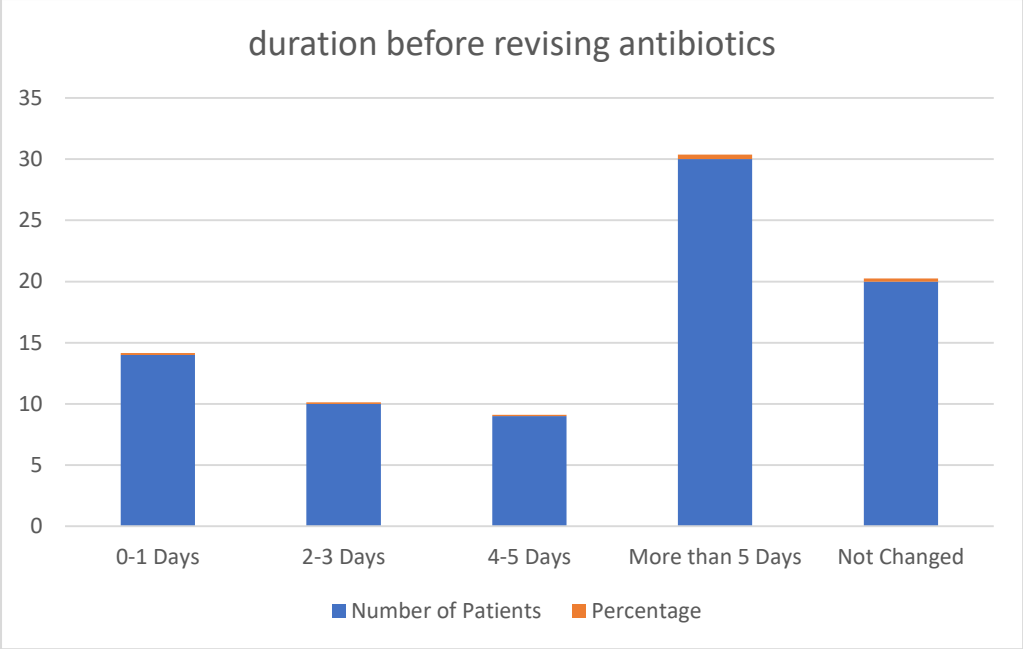

Figure 19: Duration before Changing Antibiotics after FilmArray Test.

Table 23. Antibiotic discontinuation/de-escalation

Drug	No of patients	Percentage
Meropenem	20	24%
Teicoplanin	18	21.6%
Piperacillin-tazobactam	12	14.4%
Azithromycin	19	22.8%
Doxycycline	2	2.4%
Ceftriaxone	5	6%
Voriconazole	5	6%
Fluconazole	1	1.2%
Others	7	8.4%

In the above table, we analyzed in our study that in 20 patients Meropenem was discontinued on the basis of FA resistance gene and also comparing it with the culture sensitivity report. Among 83 patients, in 19 patients, Azithromycin was stopped and in 18 patients Teicoplanin was discontinued, followed by Piperacillin and Tazobactam in 12 patients. Among 2 patients, Doxycycline was discontinued after FA results. Ceftriaxone and Voriconazole was stopped in 5 patients each. Rest had various antibiotic discontinuations. This implies the individualized approach towards selection and deselection of appropriate antibiotics.

The most common potential intervention was an appropriate antibiotic de-escalation or discontinuation, which encompassed 206 total antimicrobials (78.3% of all antimicrobials considered) in 122 individual patients (48.2% of all patients considered). These de-escalations and discontinuations resulted in a potential to reduce the duration of unnecessary antibiotic therapy by over 18,000 cumulative hours in these 122 patients.

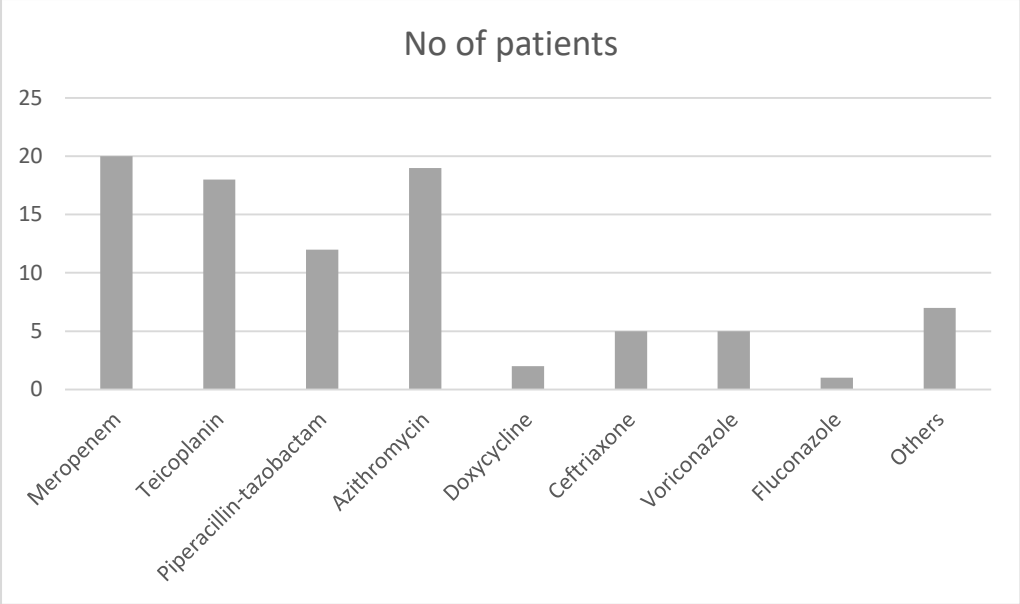

Figure 20. Antibiotic discontinuation/de-escalation

Table 24. Events during hospital stay

events	Number of Patients	Percentage
Off oxygen	13	15.6%
On NIV+oxygen support	10	12.04%
Intubation	60	72.28%
Inotropic support	10	12.04%
Tracheostomy	5	6.02%

The table depicts events among patients during hospital stay, with 60 patients (72.28%) requiring intubation during their hospital stay and 13(15.6%) patients were off oxygen during entire hospital stay. 10 patients (12.04%) required inotropic support during the stay. Only 5 patients (6.02%) underwent tracheostomy. Rest 10 patients had various levels of oxygen requirement during their stay. This data signifies the various respiratory supports during the hospital course of the patients implying individual needs and therapeutic requirements.

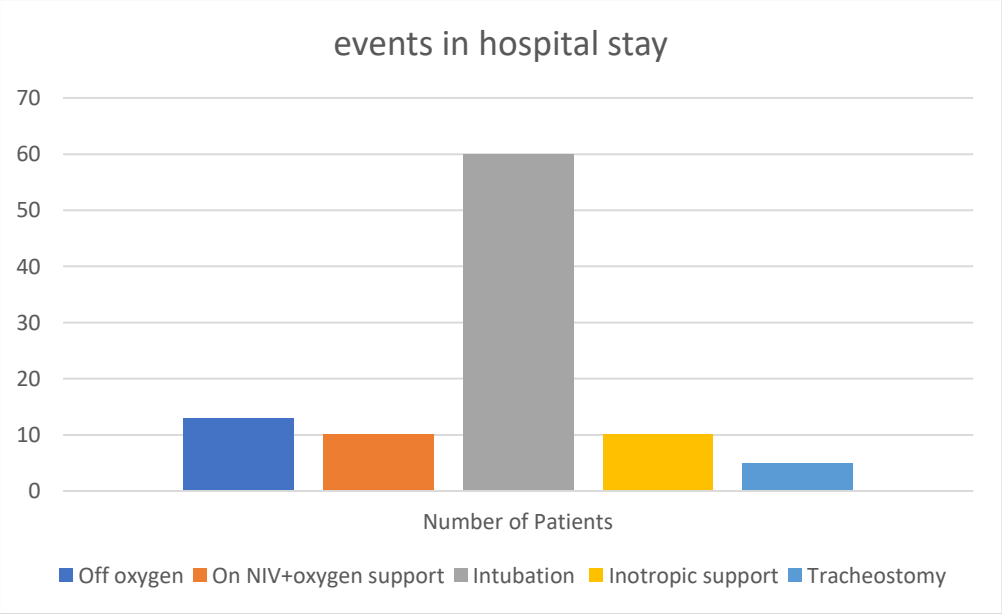

Figure 21. Events during hospital stay

Table 25: Number of days of ICU stay after film array

Number of days	Number of patients	Percentage
<1 day	6	7.22%
1-5days	16	19.27%
6-10 days	19	22.89%
11-20 days	25	30.12%
>21 days	17	20.48%

The above table shows the length of ICU stay after the film array report and changing of antibiotic regimen. Majority of the patient 25 (30.12%) had ICU stay between 11-20 days. 19 patients had reduced ICU stay of 6-10 days. 16 patients had stay of 1-5 days and 17 patients had stay of >21days. Fewer (7.22%) had least number of ICU days of <1 accounting to early death or early diagnosis and better treatment. ICU stay implies the effect of delay in Film array and appropriate tailoring of antibiotics.

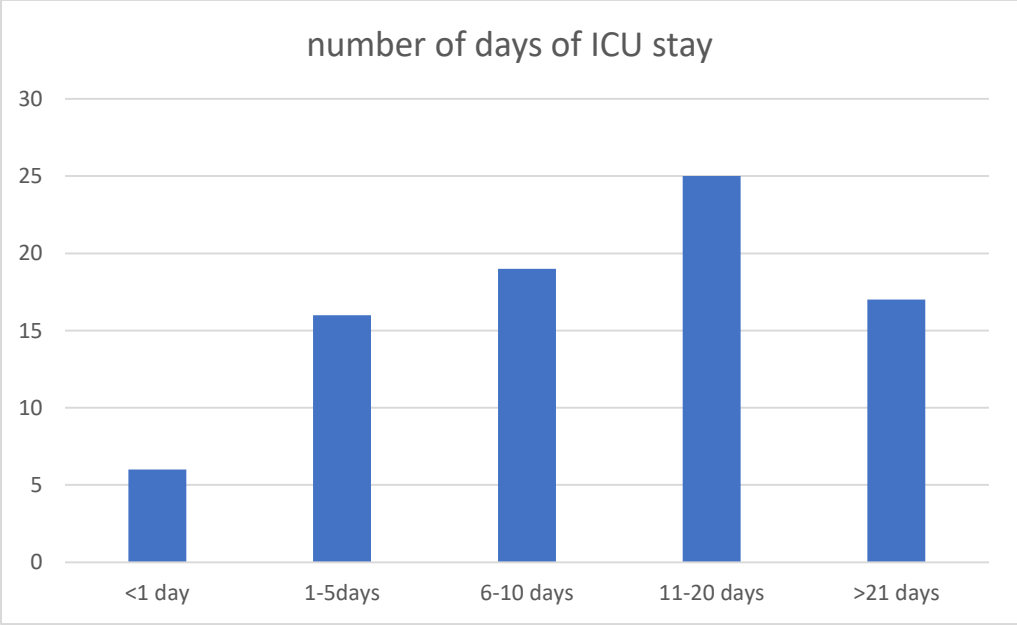

Figure 22: Number of days of ICU stay after film array

TABLE 26: CLINICAL OUTCOMES

1.INTUBATED=60	a. EXTUBATED=14	• Extubate on room air=13
		• Extubate on NIV=1
	b.REMAINED INTUBATED=46	• DAMA=29
		• Expiry=17
2.Off oxygen=13	DISCHARGED with symptomatic resolution	
3.NIV=8	a.DAMA=1	
	b.EXPIRY=1	
	c.DISCHARGED ON NIV+OXYGEN=1	
	d.DISCHARGED ON NIV WITHOUT OXYGEN=4	
	e.DISCHARGED ON ROOM AIR=1	
4.On oxygen support=2	DISCHARGED ON MINIMAL OXYGEN	

In the above table, majority patients 60(72.2%) got intubated at some point during their hospital stay, out of which 14 were successfully extubated and 13 were discharged on room air and 1 was discharged on domiciliary NIV support. Out of 60, 42 patients were still intubated

and among those, 29 patients took discharge against the medical advice and 17 expired. 13 patients were discharged with resolution of their symptoms. 8 patients were given NIV support during the stay, out of which 1 took DAMA, 1 got expired and rest were discharged. 2 patients who required high oxygen support were discharged on minimal oxygen support at home. Therefore in nutshell, 35 patients out of 83 were discharged, 30 took DAMA and 18 patients expired.

Table 27. Radiological Outcomes

Findings	Number of Patients	Percentage
Clear	22	26.5%
ARDS	22	26.5%
Pleural Effusion	14	16.8%
Consolidation	17	20.4%
Lung Collapse	3	3.6%
Others	5	6%

The table illustrates radiological improvement among patients, 22 out of 83 patients had their chest xray clear after the treatment completion. 22 patients had worsening of xray as bilateral haziness/ARDS. 14 patients (16.8%) had pleural effusion persisting in single or both the lungs. 20.4% i.e. 17 patients had patches of consolidation persisting in their cxray. Only a minority of patients 3.6% had lung collapse. Others had various outcomes as fibrosis, opacities. This signifies importance of imaging in knowing treatment status of the patient.

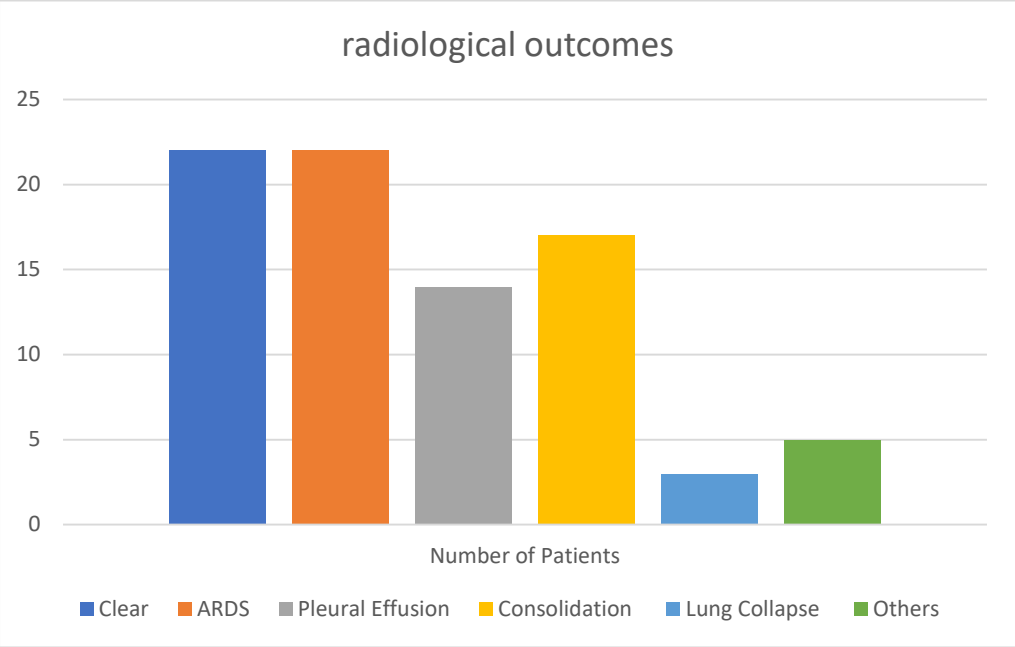

Figure 23: Radiological Outcomes

DISCUSSION

We conducted a study to assess the clinical significance of diagnosing Pneumonia, selecting appropriate antibiotics, and comparing outcomes using Film Array in comparison to standard methods. The study aimed to compare the clinical significance of diagnosing Pneumonia in patients with Film Array versus those with standard procedures, to observe improvement in antibiotic stewardship of Pneumonia between patients treated according to the Film Array test's molecular results versus those treated with standard methods, and to compare outcomes in Pneumonia patients treated according to the Film Array test versus those treated with standard methods. A total of 83 patients who were hospitalized at DMCH Ludhiana participated in the study. Clinical specimens, including endotracheal (ET) secretions, bronchoalveolar lavage (BAL), and sputum, were analyzed using a multiplex Real-Time PCR assay designed for pneumonia panels. Additionally, standard methods such as gram stain and culture sensitivity testing were employed for sputum and ET samples. The data for this study were collected from hospitalized patient populations who showed clinical features of pneumonia and X-ray changes suggestive of the condition. The study focused on comparing the efficacy of Film Array testing and traditional diagnostic approaches in managing Pneumonia cases.

The summary of patient demographics demonstrates a range of ages, reflecting the varying susceptibility to Pneumonia across different age groups. The largest proportion of patients falls within the 50 to 69-year-old range, making up 42.17% of the total population, with the highest number of individuals in the 50-59 age bracket (21.69%). Patients under 20 and those aged 80-89 make up smaller percentages at 2.41% and 6.02%, respectively. These findings emphasize the importance of considering age demographics in healthcare management and the allocation of resources within this population. In terms of gender distribution, the data shows a higher representation of males compared to females, with 52 males and 31 females among the patients.

Understanding such gender imbalances is crucial for healthcare providers to effectively tailor treatments and interventions according to the specific needs and health concerns of different gender groups. In comparison to a study conducted by **Darie[41]et al**, where the average age of the subjects was 65.9 years, and the majority were men (65%), **Sze Hwei Lee et al [42]** found that 43.9% were male and the median age was 65 years (ranging from 30 to 97 years). Similarly, a study by **Kirstine K. Søgaard et al**[49], which included 840 patients, reported a median age of 68 years and 60% of patients being male, mirroring our study's findings.

In our research, we found that dyspnea, or shortness of breath, was the most common symptom, reported by 65 patients (37.36% of total complaints). This was closely followed by fever, which affected 61 patients (35.06%). Cough was also frequently reported, with 43 patients (24.71%) experiencing this symptom. Other symptoms such as chest pain were reported by only a small percentage of patients. This breakdown provides valuable insights into the primary concerns and symptoms presented by the patient population, which can help healthcare professionals prioritize and address these issues effectively. A meta-analysis by **Pyai Htun et al[51]** suggested that clinical history and symptoms are not discriminative, but cough was found to be the most important symptom for diagnosing pneumonia in adults in a primary care setting. Tachypnea had the highest specificity, followed by pyrexia and tachycardia. According to a study by **Kirstine K. Søgaard et al**[49], fever was the initial symptom in 11% of patients.

When examining the presence of other diseases alongside a primary condition, the data reveals that diabetes (DM) and hypertension (HTN) are commonly seen, affecting 43.3% and 37.3% of patients, respectively. In this study, 13.2% of patients had CAD, 6.02% had COPD, and only 2.4% had ILD. The "OTHERS" category covers a wide range of comorbidities and is prevalent in 38.5% of patients. 24.09% of patients had no comorbidities. It is essential for healthcare providers to

be aware of these comorbidities in order to provide appropriate treatment and anticipate potential complications during the management of Pneumonia in these patients. According to **E. Blance et al**[3], cardiac diseases, including hypertension, were the most common comorbidities in patients at risk of CAP. Mortality rates increased with age and the number of comorbidities, as found by **Kirstine K. Søgaard et al**[49], who included 35% of patients with chronic pulmonary diseases and no other comorbidities.

The oxygen saturation levels of patients upon admission were analyzed in our study, revealing distinct patterns crucial for understanding their clinical status. Among the patients assessed, 7.20% had oxygen saturation levels falling within the 100-96% and 91-95% range, indicating relatively stable oxygen levels. A notable proportion, accounting for 26.50%, exhibited saturation levels between 86-90%, suggesting a moderate decrease in oxygen saturation. Our findings also showed that 21.60% of the patients presented with oxygen saturation levels between 85-80%, indicating a significant risk of hypoxemia. Additionally, 37.20% of patients had saturation levels of less than 80% on room air. These findings underscore the critical importance of closely monitoring oxygen saturation levels upon admission, as they serve as valuable indicators of respiratory function and can guide timely interventions to optimize patient care. In a study by **Sumit R Majumdar et al**[52], the mean blood oxygen saturation was 95%. 4% of patients had blood oxygen saturations of less than 90% and 7% had blood oxygen saturations of 90%-92%. In comparison, the study by **Kirstine K. Søgaard et al**[49] found that the median oxygen saturation was 94% on room air.

In our research on chest X-rays (CXRs), we observed a range of pulmonary conditions. The most frequent discovery was consolidation, found in 33.73% of cases, followed by pleural effusion (25.30%) and haziness (11.34%). ARDS was detected in 7.22% of patients, while opacities were relatively uncommon, occurring in only 4.81% of cases.

Two patients had normal chest X-rays. Only 10 patients displayed various pulmonary abnormalities such as lung collapse and surgical emphysema. These findings emphasize the intricacy and variety of respiratory conditions identified through CXR examinations in this patient group. Additionally, **Atsushi Nambu et al**[53] carried out a study wherein they determined that chest radiography is generally adequate to confirm CAP diagnosis. Specific imaging observations are linked to *Mycoplasma pneumoniae pneumonia, M. tuberculosis, Pneumocystis jirovecii pneumonia*, and certain viral pneumonia. For example, peribronchial nodules and a tree-in-bud appearance indicate infection, while the concavity of opacities, traction bronchiectasis, visualization of air bronchograms, or mild parenchymal distortion suggest organizing pneumonia.

The samples utilized for testing were mainly endotracheal secretions (ET secretions), making up 59.04% of the total. Sputum accounted for 37.35% of the samples, while bronchoalveolar lavage (BAL) made up 3.61%. The results of the Film Array test provided insights into the various pathogens affecting patients with Pneumonia. A total of 165 targets were identified on Film Array, including 116 bacteria and 49 viruses. *Acinetobacter baumannii* was the most frequently detected organism, accounting for 24.13% of bacterial targets, followed by *K. pneumoniae* at 23.2%, and *Staphylococcus aureus* and *E. coli*, each found in 13 patients, making up 11.2% of the targets. *Pseudomonas aeruginosa* accounted for 10.34%, and *H. influenzae* comprised 6.8% of the total bacterial targets. *Enterobacter cloacae* and *Streptococcus agalactiae* were found in 4.3% of cases, *Streptococcus pneumoniae* in 2.5%, and *Serratia* and *Proteus mirabilis* had the lowest percentage among the bacterial targets. Among the viral targets, *Influenzae* A was detected in 14 samples, followed by *Influenzae* B in 18.3% and *Humanenterovirus/rhinovirus* in 16.3%. *Adenovirus* was found in 10% of the total viral targets. *Coronavirus* and RSV were found in 8%, followed by *Parainfluenzae virus* in 6%, and H1N1 and *Metapneumovirus*, each making up 2% of the total viral targets. Film

Array was extremely advantageous in detecting viral targets that were not cultivable using the culture method. The study revealed that 28 patients had both bacteria and viruses, 14 patients had a single bacteria, and 16 patients had a single virus. 16 patients had more than one bacterial target in their Film Array report. Only 2 patients had multiple viruses, and 7 patients had no targets found in their Film Array report. In comparison to the study conducted by **Kirstine K. Søgaard et al**[49], PN showed 346 bacterial and 153 viral targets, with the main organism being *H. influenzae* at 13.3%, followed by *Staphylococcus aureus* at 9.1%. A study by **Jones R.N et al**[44], focusing on the etiology of HAP and VAP, identified *A. baumannii complex, K. pneumoniae*, and *S. aureus* as the three most prevalent organisms at 30.5%, 25.4%, and 20.3% respectively, along with 1 *L. pneumophilia* and 6 viruses. **Sze Hwei Lee et al**[42] found co-infection in 42.3% of specimens, with *Klebsiella* at 21% being the most common infection, followed by *Pseudomonas* at 14%, and *Acinetobacter* and *Staphylococcus* at 12% each, resulting in a PPV of 90% and NPV of 97%. They also discovered 16 viruses and the 4 CTX-M and 3 IMP/NMD/VIM genes. **Kosuke Kosai et al**[38] reported that in their study, *Pseudomonas* was the predominant bacterial target in 17 cases, followed by *Klebsiella* in 10 patients and *Acinetobacter* in 6 cases. They also found 5 cases with mecA/C and MREJ and 4 CTX-M genes. **Mitton B et al**[46] compared the performance of FA to traditional culture methods for diagnosing LRTI took 59 samples among which *A. baumannii complex* was the most frequently detected at 42.9% (18/42), followed by the *K. pneumoniae* group at 35.7% (15/42) and *S. aureus* at 28.6% (12/42). The least commonly identified targets were *K. aerogenes* at 2.4% (1/42), *S. agalactiae* at 2.4% (1/42), and *S. pyogenes* at 2.4% (1/42). Culture methods identified fewer organisms compared to the FAPP panel and failed to identify *M. catarrhalis, Proteus species, S. agalactiae*, and *S. pyogenes*. in terms of detecting antibiotic resistance, the positive and negative percent agreements were 100% and 98.5% respectively. In a study by **Faron ML et al** [43], in patients with LRTI, 57 BAL and 48 sputum were collected which were analysed using FA, out of which 17

had bacterial antigens and 9 had viral and 2 had fungal. Resistance genes detected were KPC, CTX-M, VIM, IMP, NDM, OXA-48 and mecA/C. The FAPP panel proved to be highly accurate for evaluating tracheal aspirate specimens from hospitalized patients. The variation in the organisms detected by these studies depends on the type of pneumonia (CAP/HAP/VAP), with our being a tertiary center, majority patients had received multiple hospitalisations before.

Upon subjecting the same targets to the culture method for diagnosis, it revealed that 53 cultures showed no growth, while 15 patients had *Acinetobacter baumannii* and 12 cultures showed *Klebsiella pneumoniae. Pseudomonas* was seen in 3 cultures, *Escherichia coli* was seen in 2 patients and *Enterobacter cloaca, Staphylococcus hominis, Citrobacter koseri* and *Stenotrophomonas* showed growth in one patient each. This data underscores the prevalence of negative cultures among the patients, suggesting potential implications for treatment strategies and healthcare management. It's important to note the findings from the research studies. The analysis conducted by **Kosuke Kosai et al** [38]. using the PN panel revealed a total of 97 targets, including 84 bacteria, 4 viruses, and 9 antimicrobial resistance markers from the 57 samples analyzed. However, the bacterial culture yielded only 25 bacteria and 2 resistance organisms. The PN panel demonstrated 100.0% positive agreement and 92.9% negative agreement with culture methods for bacterial detection. Additionally, in a separate study by **Kirstine K. Søgaard et al**[49], it was found that the most common bacteria detected in the culture method was *Staphylococcus aureus* (4.5%) followed by *Pseudomonas aeruginosa* (3.6%). These findings underscore the significance of negative cultures among patients, emphasizing potential implications for treatment strategies and healthcare management.

In our study, we studied the comparison between the yield of the pneumonia panel and the culture growth report. Bacterial targets were detected the majority of times on the pneumonia panel as compared to

culture growth, in 14 patients, *Acinetobacter* was found in both culture growth and pneumonia panel, in 1 patient it was positive only in culture growth and in 14 patients it was found only on pneumonia panel and was not found on culture growth. *Klebsiella pneumoniae*- in 8 patients the organism was found in both culture and pneumonia panel, in 4 patients only on culture method and 19 patients on pneumonia panel. *Staph aureus* was seen in film array in 13 patients. *E. coli* was detected in 1 patient in both pneumonia panel and culture growth, in 2 patients only in culture and 12 patients only in the pneumonia panel. All the viruses detected were not found in any culture growth but only found in the pneumonia panel thus implying the high diagnostic accuracy of this method. FA is 87.6% specific for bacteria and highly specific for viruses. It has a 20% PPV. 100% NPV for bacteria. 78.1% sensitive for bacteria. **Blake W Buchan et al[45]** studied the PPA (positive percentage agreement) of the PN panel for the detection of bacterial targets was 96.2% (75/78) and NPA (negative percentage agreement) was 98.1% (3,734/3,807) with routine culture reports. In their study 3 culture-positive, PN panel-negative targets were detected at a low quantity which included the first *E. coli* reported at 10^3 CFU/ml in culture also containing, *S. aureus* at 10^4 CFU/ml and *K. pneumoniae* at 10^3 CFU/ml (both *S. aureus* and *K. pneumoniae* were detected by the PN panel), second *S. aureus* reported at 10^3 CFU/ml in culture (the PN panel detected *Streptococcus agalactiae*), and third *P. aeruginosa* reported as “few” in culture (the PN panel was negative for all targets). In the study by **Kosuke Kosai et al [38]**, in 24 samples multiple pathogens were detected, 11 samples had 2 pathogens each and 1 sample had 6 pathogens. **Caitlin N. Murphy et al[48]** in their study found an overall sensitivity of 75%-100% for sputum samples and 85%-100% for BAL, whereas the specificity ranged from 89-100% in both. Atypical bacteria couldn’t be read by the qRefCx comparator method. **Kirstine K. Søgaard et al[49]** took 1078 BAL samples, 36% of samples had bacterial growth in FA and 16% had bacterial growth in culture media. The overall sensitivity and specificity of FA was high and PPV was very low in their study. In a study by **Nathan Peiffer-Smadja et**

al[27] 19Total targets detected were 112 out of which 90 were bacterial targets with the detection of 5 CTX-M genes, 3 NDM and 1 OXA-48 LIKE genes. 2 patients had Legionella growth on the culture media. This multiplex PCR had a sensitivity of 80% and specificity of 99%.

In order to choose the right antibiotics for treatment, we compared the resistance genes and culture sensitivity. *Acinetobacter baumannii* patients who were resistant to carbapenemases showed sensitivity to colistin in the culture, so the treatment was adjusted accordingly. Patients with *E. coli* carrying resistance genes CTX-M, NDM, VIM, and OXA-48 LIKE were found to be sensitive to colistin, amikacin, gentamicin, and tigecycline based on the culture results. Similarly, K. pneumoniae with resistance genes IMP, NDM, CTX-M, OXA-48 LIKE, and VIM showed sensitivity to colistin, amikacin, and gentamicin in culture. Out of 262 targets, the NDM gene was present in 80 (30.5%) bacterial targets, followed by CTX-M and OXA-48 LIKE in 61 (23.2%) bacterial targets. 40 bacterial targets carried the resistance gene VIM, while 18 targets showed the presence of IMP, and only 2 had the KPC gene, which was not detected on culture media due to the initial empirical antibiotics given. In a study conducted by **Blake W Buchan et al**[45], 42 specimens were found to contain S. aureus using the PN panel, and out of those, 21 (50%) were confirmed positive for S. aureus in both FA and cultures. The PN panel showed 81.8% sensitivity (9/11) and 85.7% specificity (6/7) in identifying MRSA by detecting mecA/C and MREJ gene in 18 isolates. The FA panel indicated the presence of a carbapenemase gene (KPC, NDM, VIM, IMP, or OXA-48) or an ESBL gene (CTX-M) in 4 out of 53 specimens containing a bacterial target. Among these, two specimens tested positive for KPC and one each for NDM and CTX-M. A phenotypically carbapenem-resistant organism was reported in routine culture in both specimens that tested positive for KPC. When compared to the study by **Kirstine K. Søgaard et al**[49]**,** 5 bacteria were identified with a CTX-M gene, and 6 had mecA/C and MREJ genes, as *H. influenzae* and *Staphylococcus aureus* were the predominant bacteria found in this study.

Upon the implementation of revisions in antibiotic prescriptions following the FA report analysis, notable changes in treatment strategies were observed. A quarter of the patients (24.10%) experienced no alterations in their antibiotic regimen, suggesting that the initial empirical treatment was based upon the clinical judgement. However majority of patients (75.90%) underwent various other antibiotic modifications, reflecting a personalized approach to treatment adjustments tailored to individual patient profiles and pathogen susceptibilities identified through molecular testing. This nuanced approach underscores the value of incorporating rapid diagnostic technologies like FilmArray in clinical decision-making, facilitating more precise and effective antibiotic stewardship practices.

The most commonly prescribed treatment in our research was a combination of Meropenem and teicoplanin, accounting for 56.63% of cases. This combination is likely due to its broad-spectrum coverage and effectiveness against severe bacterial infections commonly found in pneumonia cases. Following this, 22.89% of cases received a combination of meropenem, teicoplanin, and azithromycin, which suggests an effort to cover both bacterial and atypical pathogens often associated with pneumonia. A smaller group, comprising 12.05% of cases, received a regimen of piperacillin, tazobactam, and azithromycin, indicating a personalized approach based on individual patient factors or antimicrobial stewardship considerations. The remaining 8.43% of cases received other antibiotic combinations, showing the diversity of treatment approaches used in clinical practice. In discussing the empirical antibiotic treatment used for patients in our study, we observed distinct patterns in antibiotic selection. In a study by **Kirstine K. Søgaard et al**[49], amoxicillin-clavulanic acid was initiated in 33% of cases, piperacillin and tazobactam in 46% of cases, and meropenem was given as an empirical antibiotic in 14% of patients. Following the analysis of the FA report, significant changes in treatment strategies were observed in our study. A quarter of the patients (24.10%) experienced no changes in their antibiotic regimen,

suggesting that the initial empirical treatment was based on clinical judgment. However, the majority of patients (75.90%) underwent various antibiotic modifications, indicating a personalized approach to treatment adjustments based on individual patient profiles and pathogen susceptibilities identified through molecular testing. This nuanced approach underscores the value of incorporating rapid diagnostic technologies like FilmArray in clinical decision-making, facilitating more precise and effective antibiotic stewardship practices. Based on results from FA, target organism and resistance gene, the duration after which antibiotics were changed after the FilmArray report showed that in the majority of patients (36.14%), the antibiotics were revised after 5 days. In 14 patients, antibiotics were escalated within 1 day of reporting. In 10 patients (12.04%), antibiotics were changed within 2-3 days of the FilmArray reporting. We found that in 20 patients, Meropenem was discontinued based on the FA resistance gene and in comparison with the culture sensitivity report. Among 83 patients, in 19 patients, Azithromycin was stopped and in 18 patients, Teicoplanin was discontinued, followed by Piperacillin and Tazobactam in 12 patients. Among 2 patients, Doxycycline was discontinued after FA results. Ceftriaxone and Voriconazole were stopped in 5 patients each. The rest had various antibiotic discontinuations. This implies an individualized approach toward the selection and deselection of appropriate antibiotics. In a study conducted by **Josep Ferrer et al**[47], among the 99 patients undergoing evaluation, 44 tested positive for one or more bacterial targets and 55 did not have any targets seen. For those testing positive with FA-PP, antibiotic prescription involving either de-escalation, escalation, or continuation following the report of the FA-PP results was deemed suitable in 27 out of 44 cases. Regarding those testing negative with FA, decisions were made in 22 out of 55 accordingly. These changes were inadequate as MRSA antibiotic coverage (36/50) was not discontinued. In 29 out of 36 cases, the antibiotic that was not withdrawn was linezolid, and in 7 cases, it was Ceftaroline. Fluoroquinolones, Amikacin, Ceftazidime-Avibactam, or other antibiotics in smaller proportions were not withdrawn after the FA

report. Importantly, modifications in antibiotic therapy based on FA results were implemented based on the attending physician's criteria and were not related to the result of the FA. **Blake W. Buchan et al**[45] discontinued antimicrobials in 122 patients (48.2%) out of 206 total antimicrobials, reducing the unnecessary burden on treatment regimens. **Trevor C. Van Schooneveld et al**[50] found in their study that antibiotic changes were made in 82% of patients out of 313 patients within 23 hours of admission and were de-escalated within 18 hours. Anti-MRSA and anti-pseudomonal drugs were discontinued within 13 hours. Also, the duration of vancomycin, azithromycin, and metronidazole was reduced. **Darie**[41] **et al** found in their study that the duration of inappropriate antibiotics was decreased by 38.6 hours in 45% of cases after the FA report.

After identifying the responsible organism, antibiotics were used based on the resistance gene. The majority of patients (30.12%) had an ICU stay of 11-20 days, followed by 19 patients with a stay of 6-10 days, and 17 patients (20.48%) had a prolonged ICU stay of more than 21 days. Only 6 patients had the shortest stay of less than 1 day, including those who did not survive. 16 patients stayed for 16 days in the ICU. Our findings revealed that in patients whose antibiotic treatment was adjusted based on a specific report, the majority of patients (53) were intubated at some point during their hospital stay. Out of those, 12 were successfully removed from the ventilator and 11 were discharged breathing room air, while 1 was discharged with domiciliary NIV support. Out of the 53 patients, 41 were still intubated, and among those, 28 patients chose to discharge themselves against medical advice, and 13 did not survive. 3 patients were discharged with resolved symptoms. 6 patients received NIV support during their stay, of which 1 chose to discharge themselves against medical advice, 1 did not survive, and the rest were discharged. 1 patient who initially required high oxygen support was discharged with minimal oxygen support at home. Among the 20 patients for whom antibiotics were not adjusted after a specific report, 1 was discharged needing nasal

oxygen support at home, 2 with domiciliary NIV, 7 were intubated, out of which 2 were removed from the ventilator and 4 did not survive, and 1 patient chose to discharge themselves against medical advice. 9 patients were discharged breathing room air. In summary, out of 83 patients, 35 were discharged, 30 chose to discharge themselves against medical advice, and 18 did not survive. Our investigation also evaluated the radiological outcomes among the study cohort. 22 out of 83 patients had clear chest X-rays after completing treatment, 22 patients had worsening chest X-rays showing bilateral haziness/ARDS, and 14 patients (16.8%) had persistent pleural effusion in one or both lungs. A total of 17 patients (20.4%) had patches of consolidation persisting in their chest X-rays. A small percentage of patients (3.6%) had a lung collapse, while others had various outcomes such as fibrosis and opacities. This emphasizes the importance of imaging in understanding the patient's treatment status. These findings indicate that a significant proportion of pneumonia patients show positive radiological responses to treatment, demonstrating the effectiveness of the interventions used. However, it is important to recognize that some patients may not show radiological improvement despite clinical progress, highlighting the complex nature of disease progression and treatment response. A mean hospital stay of 12 days and mortality of 9% was observed in patients included in a study by **Kirstine K. Søgaard et al**[49]. In the study conducted by **Darie**[41] **et al** 8% of cases resulted in mortality.

SUMMARY & CONCLUSION

SUMMARY

The study aimed to evaluate the effectiveness of diagnostic techniques, understand patient demographics and outcomes, and investigate treatment reliability for pneumonia. The goal was to improve the accuracy of diagnosing pneumonia and enhance patient outcomes using multiplex PCR Pneumonia Panel. These panels were effective in detecting various bacterial and viral targets, especially in identifying organisms that did not grow on the panels. After evaluating the organisms, antibiotic treatment was based on the resistance gene identified on the panels and the sensitivity pattern on culture media. This approach facilitated early discontinuation of inappropriate antibiotics and cessation of antibiotics in cases involving viral targets. Patients treated based on the panel findings showed clinical and radiological improvements. The timely inclusion of this approach in routine pneumonia diagnosis can help guide the use of appropriate antibiotics and reduce antibiotic resistance.

CONCLUSION

- The majority of patients belong to the 50-69 age group, demonstrating the need for specific healthcare approaches targeted at older adults.
- There is a higher occurrence of male patients, signifying the importance of considering gender-specific health factors and interventions.
- Common patient symptoms like difficulty breathing, high body temperature, and cough have been identified, necessitating focused approaches to diagnosis and treatment.
- The most common coexisting medical conditions are diabetes and hypertension, underscoring the need for comprehensive programs to manage chronic diseases.

- A significant number of patients exhibited critical oxygen saturation levels upon admission, emphasizing the urgency of immediate clinical assessments and interventions.
- The most prevalent auscultation findings include crackling sounds, indicating widespread respiratory issues within the patient group.
- Various pulmonary conditions have been identified through CXR, highlighting the complexity of respiratory illnesses and the need for comprehensive pulmonary care.
- The majority of samples for testing consist of ET secretions, reflecting a large number of cases of hospital-acquired pneumonia or ventilator-associated pneumonia.
- FA was conducted after a few days of admission for most patients, emphasizing the prior use of antibiotics or nosocomial infection.
- Results from the FilmArray test show a diverse spectrum of pathogens, underscoring the importance of accurate pathogen detection for effective treatment.
- The significant presence of a resistance gene in the patient population underscores the challenge of antibiotic resistance and the need for treatment strategies focused on resistance.
- Gram stain and culture did not produce sufficient growth, indicating the use of empirical antibiotics prior to culture.
- Empirical antibiotic treatment primarily involves meropenem and teicoplanin, suggesting a high likelihood of sepsis present in the cases.
- Following the FilmArray report, there was a substantial adjustment made in antibiotic prescriptions to tailor the approach to antimicrobial therapy based on specific pathogen identification.
- Antibiotics were continued along with antivirals in cases with only viral targets due to the presence of superadded sepsis.
- Clinical and radiological improvements in half of the patients indicate effectiveness of the treatments applied, though variability in response necessitates personalized care strategies.

RECOMMENDATION:

- Increase the deployment of the FilmArray system in more hospitals to accelerate the diagnosis and treatment of Pneumonia, leveraging its demonstrated effectiveness in improving clinical outcomes.
- Incorporate the results of the FilmArray test into clinical decision-making processes to bolster antimicrobial stewardship and decrease the use of broad-spectrum antibiotics.
- Conduct training sessions for healthcare providers on the utilization and interpretation of FilmArray results to ensure its optimal utilization and integration into standard care practices.
- Promote further research on the FilmArray system with a more extensive and more diverse patient population to validate and broaden the findings from this study.
- Create guidelines for the prompt management of Pneumonia that include rapid diagnostic tests like the FilmArray to standardize care across healthcare settings.
- Oversee and assess the long-term outcomes of patients treated based on FilmArray test results to evaluate the impact on antibiotic resistance patterns and patient morbidity and mortality.
- Cultivate interdisciplinary collaboration among laboratory technicians, physicians, and pharmacists to improve the comprehensive management of Pneumonia, ensuring that all healthcare providers are in harmony in the use of advanced diagnostic tools.
- Champion the incorporation of rapid diagnostic testing in national and international guidelines for the management of pneumonia to ensure widespread adoption and standardization of care practices.
- Assign resources for continuous training and support for healthcare facilities incorporating the FilmArray system to ensure continued quality of care and adherence to best practices.

- Conduct analyses of the costs and benefits of integrating rapid diagnostic tools like the FilmArray system in different healthcare settings to inform policy decisions and resource allocation.

LIMITATIONS:

- The study was conducted in a single centre (DMCH Ludhiana), which may limit the generalizability of the results to other settings or populations.
- The study period was limited to one year, which may not adequately capture seasonal variations in the incidence of Pneumonia or the variety of pathogens that can cause it throughout different times of the year.
- The exclusion of outpatients and patients already on antibiotics may lead to a selection bias, as these groups could have differing baseline characteristics and treatment responses.
- Less preference is given to choosing the film array over standard culture due to its high cost.
- Reliance on routine clinical specimens like ET secretions, BAL, and sputum may introduce variability in the quality of the samples, potentially affecting the sensitivity and specificity of both the FilmArray test and standard methods.
- The use of the Kolmogorov-Smirnov test and Fisher exact test is appropriate for the data analysis, but the interpretation of these statistical methods requires careful consideration, especially in the context of multiple comparisons and small sample sizes.
- The FilmArray test, while advanced, may not detect all pathogens or resistance genes, and its performance compared to emerging diagnostic technologies was not evaluated.
- The timing of getting the film array was variable due to the individualized approach in treatment that affects the outcome.

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				ADDITIONAL INFORMATION			Visitation Details			EXAMINATION FINDINGS	
Sr No	MRD	Age(YRS)	Gender	COMPLAINS	COMORBIDITIES	SATURATION	ADMISSION DATE	DATE OF DISCHARGE	Result	AUSCULTATION	CXR
1	1453273	18	F	FEVER, DYSPNEA	NO COMORBIDITY	72% ON RA	29/01/23	02/03/23	DISCHARGE	BRONCHIAL BREATHING	ARDS
2	1473509	42	F	COUGH, DYSPNEA	NO COMORBIDITY	85% ON RA	02/03/23	18/03/23	DISCHARGE ON NIV	B/L RHOCHI	B/L OPACITIES LL
3	1390373	47	M	DYSPNEA , ALTERED SENSORIUM	NASAL ANGIOFIBROMA	80%ON RA	02/03/23	10/03/23	DAMA	B/L COARSE CREPTS	RIGHT CP ANGLE BLUNT
4	1471395	63	M	DYSPNEA,WEIGHT LOSS, FEVER	DM,HTN	87% ON RA	27/02/23	17/03/23	DAMA	B/L CREPTS	RIGHT CP ANGLE BLUNT
5	957093	41	M	FEVER,COUGH,SORE THROAT,DYSPNEA	NO COMORBIDITY	88% ON RA	09/01/23	18/01/23	DISCHARGE	B/L RHOCHI	LEFT LOBE CONSOLIDATION
6	1442804	46	F	FEVER,COUGH	DM	87% ON RA	06/01/23	13/01/23	DISCHARGE ON NIV	B/L COARSE CREPTS	RIGHT PLEURAL EFFUSION
7	1448452	57	M	FEVER,COUGH,DYSPNEA	NO COMORBIDITY	40%ON RA	19/01/23	04/02/23	DAMA	B/L INSPIRATORY CREPTS	PATCHY CONSOLIDATION
8	1445555	71	M	DYSPNEA,FEVER	DM	90%ON RA	13/01/23	27/01/23	DAMA	B/L NVBS	CLEAR
9	1478579	20	F	DYSPNEA,COUGH,SORE THROAT	NO COMORBIDITY	88% ON RA	11/03/23	16/04/23	DISCHARGE ON NRBM+VENTURI	B/L COARSE CREPTS	B/L PLEURAL EFFUSION
10	1495206	68	M	FEVER	DM,HTN,CAD	84% ON RA	07/04/23	17/04/23	DISCHARGE	B/L COARSE CREPTS	LEFT UL CAVITATORY CONSOLIDATION
11	1418303	35	M	FEVER,DYSPNEA	NO COMORBIDITY	85% ON RA	21/11/22	02/01/23	DISCHARGE	B/L COARSE CREPTS	ARDS, B/L PATCHES
12	1472301	52	M	FEVER,DYSPNEA	DM,HTN	76% ON RA	01/03/23	09/03/23	DISCHARGE	B/L CREPTS	RIGHT LUNG COLLAPSE
13	264953	26	M	DYSPNEA,GASPING	BA	50% ON RA	05/05/23	17/05/23	DAMA	B/L RHONCHI	SURGICAL EMPHYSEMA
14	1324791	18	M	FEVER,DYSPNEA,COUGH	SEIZURE DISORDER	90% ON RA	23/05/23	05/06/23	DISCHARGE	NVBS	B/L PLEURAL EFFUSION
15	1523677	21	M	DYSPNEA,COUGH	NO COMORBIDITY	89% ON RA	25/05/23	08/06/23	DISCHARGE	B/L COARSE CREPTS	B/L OPACITIES
16	1004498	85	M	DYSPNEA,DRY COUGH	DM,OLD CVA	84% ON RA	27/05/23	01/06/23	EXPIRED	B/L FINE CREPTS	B/L CP ANGLE BLUNT
17	1526330	55	M	DYSPNEA, PRODUCTIVE COUGH	OLD PULMONARY KOCHS	88% ON RA	30/05/23	12/06/23	DISCHARGE	B/L CREPTS AND RHOCHI HEARD	B/L OPACITIES, RIGHT MILD PLEURAL EFFUSION
18	1530207	53	M	FEVER	DM, HTN	96% ON RA	05/06/23	20/06/23	DAMA	B/L BASAL CREPTS	B/L PLEURAL EFFUSION
19	993180	55	F	DYSPNEA, COUGH	DM, HTN	73% ON RA	18/04/23	30/04/23	EXPIRED	B/L BASAL CREPTS	CLEAR
20	1153694	66	F	FEVER,DYSPNEA,DRY COUGH	HTN, DEPRESSIVE ILLNESS	96% ON RA	04/03/23	18/03/23	DISCHARGE	LEFT>RIGHT CREPTS	B/L LL CONSOLIDATION
21	1477587	29	F	DYSPNEA, COUGH	HYPOTHYROIDISM, DVT	85% ON RA	09/03/23	21/03/23	DISCHARGE	B/L CREPTS	B/L CONSOLIDATION
22	1481656	66	F	FEVER, DYSPNEA	HTN	98% ON RA	15/03/23	23/03/23	DISCHARGE	B/L RHOCNCHI	B/L PATCHY CONSOLIDATION IN LL
23	1486636	46	M	FEVER, PRODUCTIVE COUGH	DM	91% ON RA	24/03/23	28/03/23	DISCHARGE	NVBS	RIGHT MILD PLEURAL EFFUSION
24	30484	64	F	FEVER, DYSPNEA	DM, HTN	84% ON RA	04/10/22	17/10/22	DISCHARGE	B/L FINE INSPIRATORY CREPTS UL>LL	PROMINENT BV MARKINGS
25	1442527	67	F	CHEST DISCOMFORT AND PAIN	HTN, CAD EF 36%	95% ON RA	06/01/23	23/01/23	DISCHARGE	B/L CREPTS AND RHONCHI	B/L HAZINESS
26	872071	75	F	DYSPNEA, CHEST PAIN, COUGH	DM, HTN	98% ON RA	14/01/23	25/01/23	DISCHARGE	NVBS	PROMINENT BV MARKINGS
27	1455152	34	M	FEVER, DYSPNEA, PRODUCTIVE COUGH	NO COMORBIDITY	96% ON RA	01/02/23	08/02/23	DISCHARGE	B/L BRONCHIAL BREATHING	PROMINENT BV MARKINGS
28	1436051	21	M	FEVER	NO COMORBIDITY	90% ON RA	22/12/22	07/01/23	DAMA	B/L AE DECREASED	LEFT LL CONSOLIDATION
29	1542327	20	M	FEVER, DYSPNEA, LOOSE STOOLS	NO COMORBIDITY	83% ON RA	26/06/23	12/08/23	DISCHARGE	B/L CREPTS	LEFT CONSOLIDATION
30	1468887	48	M	FEVER, COUGH	DM	96% ON RA	23/02/23	11/03/23	DISCHARGE	DECREASED AE LEFT SIDE	LEFT MILD PLEURAL EFFUSION
31	1596894	55	F	FEVER, PRODUCTIVE COUGH, DYSPNEA	DM, HTN, CAD	84% ON RA	26/08/23	03/10/23	EXPIRED	B/L CREPTS	ARDS
32	1640035	44	M	FEVER, DYSPNEA	DM, HTN	70% ON RA	18/12/22	01/01/23	DISCHARGE	B/L AIR ENTRY HEARD, B/L RHONCI	B/L CONSOLIDATION
33	1642389	65	F	FEVER, COUGH, DYSPNEA	DM, HTN, CKD	78% ON RA	22/12/22	26/12/22	DAMA	B/L CREPTS	ARDS
34	859282	63	M	FEVER, COUGH, DYSPNEA, PEDAL EDEMA	HTN, ICMP, LBBB, AF	GASPING	25/08/23	21/09/23	DISCHARGE	B/L CREPTS	B/L MINIMAL PLEURAL EFFUSION
35	1623259	23	F	FEVER, COUGH, DYSPNEA, CHEST PAIN	NO COMORBIDITY	93% ON RA	14/09/23	29/09/23	DISCHARGE	B/L AE DECREASED ON BASES	B/L PLEURAL EFFUSION
36	204048	81	M	FEVER, PRODUCTIVE COUGH	DM, HTN, CAD POST PTCA	88% ON RA	04/09/23	27/09/23	EXPIRED	B/L BASAL CREPTS	PATCHY CONSOLIDATION
37	1647164	38	M	FEVER, COUGH, DYSPNEA	HTN, POST COVID	80% ON RA	02/01/23	22/01/23	DISCHARGE	B/L AIR ENTRY HEARD	LEFT PLEURAL EFFUSION
38	1541629	67	M	FEVER, DYSPNEA	DM, CAD POST PTCA	80% ON RA	06/09/23	23/09/23	DAMA	B/L AIR ENTRY HEARD	LEFT PLEURAL EFFUSION
39	1595646	24	F	FEVER, COUGH, GASPING	NO COMORBIDITY	58% ON RA	24/08/23	08/09/23	DISCHARGE	B/L COARSE CREPTS	ARDS
40	1476947	85	F	FEVER, COUGH, DYSPNEA	OLD PULMONARY KOCHS, COPD, HTN	82% ON RA	09/03/23	17/03/23	DISCHARGE	B/L RHONCHI	B/L CP ANGLE BLUNT
41	1549153	76	M	FEVER, DYSPNEA	DM, PSVT	88% ON RA	08/07/23	30/07/23	EXPIRED	B/L CREPTS	B/L MODERATE PLEURAL EFFUSION
42	1643768	51	M	DYSPNEA, FEVER, PRODUCTIVE COUGH	DM, HTN	72% ON RA	25/09/23	27/09/23	EXPIRED	B/L CREPTS	ARDS
43	104545	63	F	DYSPNEA	DM, CAD POST PTCA	78% ON RA	13/08/23	23/08/23	EXPIRED	B/L CREPTS	B/L CONSOLIDATION
44	696374	80	M	FEVER, DYSPNEA	HTN, COAD, HYPOTHYROIDISM	86% ON RA	05/07/23	13/07/23	DAMA	B/L CREPTS	RIGHT UPPER LOBE PATCH
45	1600035	25	M	FEVER, DYSPNEA	NO COMORBIDITY	84% ON RA	01/09/23	08/09/23	DAMA	B/L CREPTS	B/L CONSOLIDATION
46	1614830	40	F	FEVER, DYSPNEA	DM, HTN	84% ON RA	28/08/23	03/09/23	EXPIRED	B/L RHONCHI AND CREPTS	ARDS
47	1599887	52	M	FEVER	DM	71% ON RA	30/08/23	23/09/23	DAMA	B/L CREPTS	LEFT LOWER ZONE HAZINESS
48	1470586	33	F	FEVER, PRODUCTIVE COUGH	HYPOTHYROIDISM	92% ON RA	27/02/23	07/03/23	DISCHARGE	B/L AIR ENTRY HEARD	B/L CONSOLIDATION
49	57301	79	M	FEVER, PRODUCTIVE COUGH	DM, HTN, COAD, CAD	90% ON RA	18/10/22	20/10/22	DISCHARGE	B/L AIR ENTRY HEARD	LEFT CP ANGLE BLUNTING
50	1447506	25	F	FEVER, DYSPNEA	NO COMORBIDITY	88% ON RA	22/04/23	25/04/23	DISCHARGE	B/L CREPTS	B/L OPACITIES
51	1410992	53	M	DYSPNEA, PRODUCTIVE COUGH, FEVER	SARCOIDOSIS, ILD	73% ON RA	08/11/22	19/11/22	DAMA	B/L AIR ENTRY DECREASED	B/L CONSOLIDATION
52	1470426	49	F	FEVER, COUGH, DYSPNEA	DM	58% ON RA	25/02/23	03/03/23	DAMA	B/L CREPTS, B/L BRONCHIAL SOUNDS	RIGHT MIDDLE LOBE CONSOLIDATION
53	1473465	60	M	COUGH, DYSPNEA	DM, HTN, CAD	87% ON RA	02/03/23	08/03/23	DAMA	B/L CREPTS	B/L LOWER ZONE CONSOLIDATION
54	1287339	63	M	FEVER, DYSPNEA, PRODUCTIVE COUGH	DM, HTN, CKD	86% ON RA	12/02/23	24/02/23	DISCHARGE	B/L CREPTS	B/L LOWER ZONE CONSOLIDATION
55	1332477	65	M	FEVER, COUGH, DYSPNEA	PLHIV	GASPING	29/09/22	09/10/22	DAMA	B/L AIR ENTRY DECREASED	B/L OPACITIES
56	1485302	55	F	FEVER	HTN, SEIZURE	80% ON RA	22/03/23	03/04/23	DAMA	B/L CREPTS	B/L CONSOLIDATION
57	1355061	25	F	FEVER	HTN	80% ON RA	31/08/22	11/10/22	DAMA	B/L AIR ENTRY DECREASED	B/L CP ANGLE BLUNT
58	1391288	52	F	FEVER, COUGH, DYSPNEA	DM	78% ON RA	03/10/22	18/10/22	DAMA	B/L AIR ENTRY DECREASED	B/L CONSOLIDATION
59	1374014	54	F	FEVER	ILD	82% ON RA	05/09/22	13/10/22	DAMA	B/L CREPTS	B/L HAZINESS
60	398237	67	M	FEVER, DYSPNEA	DM, COPD	GASPING	05/11/22	26/12/22	DAMA	B/L BRONCHIAL BREATHING	INCREASED BRONCHOVESICULAR MARKINGS
61	1416415	27	M	FEVER, DYSPNEA	BRONCHIAL ASTHMA, OLD KOCHS	90% ON RA	18/11/22	29/12/22	DAMA	B/L RHONCHI	RIGHT UPPER LOBE COLLAPSE
62	1421117	44	M	DYSPNEA	HTN, OLD KOCHS, SEIZURE	GASPING	26/11/22	27/11/22	DAMA	B/L CREPTS	B/L PLEURAL EFFUSION
63	1426846	58	F	COUGH, DYSPNEA	IBD	85%ON RA	05/12/22	25/12/22	DAMA	B/L CREPTS	B/L HAZINESS
64	1126755	67	M	DYSPNEA	DM, HTN, CKD, CAD	GASPING	29/11/22	29/12/22	DAMA	RIGHT AIR ENTRY DECREASED	RIGHT LOWER ZONE PATCH
65	1355780	61	M	FEVER, DYSPNEA	DM, HTN	90% ON RA	30/08/22	12/10/22	DISCHARGE	B/L RHONCHI	INCREASED BRONCHOVESICULAR MARKINGS
66	1355790	50	M	FEVER, DYSPNEA	DM	70% ON RA	31/08/22	15/09/22	EXPIRED	B/L CREPTS	LEFT PLEURAL EFFUSION
67	1347160	35	F	FEVER, PRODUCTIVE COUGH, DYSPNEA	POST LSCS	76% ON RA	08/08/23	11/08/23	DAMA	B/L CREPTS AND RHONCHI	B/L LOWER ZONE HAZINESS
68	56623	57	M	DYSPNEA	DM, CLD	84% ON RA	12/12/22	24/12/22	DAMA	RIGHT AIR ENTRY DECREASED	RIGHT MIDDLE LOBE CONSOLIDATION
69	1416294	36	M	FEVER, DYSPNEA, CHEST PAIN	NO COMORBIDITY	75% ON RA	17/11/22	23/12/22	DAMA	B/L AIR ENTRY DECREASED	B/L MINIMAL PLEURAL EFFUSION

	IMAGING					MIC
Sr No	MRD	CT CHEST	DAYS AFTER WHICH FILM ARRAY WAS DONE	FILM ARRAY	SAMPLE USED	RESISTANCE GENE
1	1453273	-	1	ACINETOBACTER 105, K. PNEUMONIA 104	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
2	1473509	CAVITATORY CONSOLIDATION WITH INFECTIVE BRONCHIOLITIS	5	E.COLI 107, K.PNEUMONIAE 1107, P.AERUGINOSA 107, ACINETOBACTER 105, INFLUENZAE B	SPUTUM	CTX-M, NDM, VIM, OXA-48 LIKE
3	1390373	LARGE PNEUMONIC CONSOLIDATION RIGHT LUNG	5	K. PNEUMONIA 107, STAPH AUERUS 107, STREP AGALACTIAE 107, E.COLI 105, ADENOVIRUS	BAL	IMP,NDM,CTX-M,OXA-48LIKE,VIM,MREJ,mecA/C
4	1471395	PERIBRONCHIAL CONSOLIDATION-PCP	13	K.PNEUMONIAE 107	BAL	NDM, CTX-M, OXA-48 LIKE
5	957093	MULTIFOCAL AREAS OF CONSOLIDATION IN B/L LUNGS	2	INFLUENZAE B	SPUTUM	-
6	1442804	B/L BRONCHOPNEUMONIA	7	STAPH.AUREUS 104, INFLUENZAE A	SPUTUM	-
7	1448452	VIRAL PNEUMONIAE	12	K.PNEUMONIAE 104	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
8	1445555	-	6	STAPH.AUREUS 107, H.INFLUENZAE 105, ACINETOBACTER 104, CORONAVIRUS,INFLUENZAE B	SPUTUM	NDM, CTX-M, mecA/C,MREJ,VIM
9	1478579	ARDS+VIRAL ETIOLOGY	14	RSV	SPUTUM	-
10	1495206	LARGE CAVITATORY CONSOLIDATION LEFT UL	8	K.PNEUMONIAE 107, P.AERUGINOSA 106, STAPH.AUREUS 104	ET SECRETION	NDM,CTX-M,mecA/C,MREJ,OXA-48 LIKE,VIM
11	1418303	-	1	ACINETOBACTE 107, P. AERUGINOSA 105, INFLUENZAE A	ET SECRETION	NDM
12	1472301	RIGHT LUNG PATCHY,GGOS WITH RETICULATIONS	2	K.PNEUMONIAE 104, E.COLI 104, STAPH.AUREUS 104, ENTEROBACTER CLOACAE 104	SPUTUM	NDM,CTX-M,OXA-48 LIKE,VIM
13	264953	-	8	STAPH.AUREUS 104, ADENOVIRUS	ET SECRETION	NDM, CTX-M, VIM
14	1324791	NECROTISING CONSOLIDATION IN B/L LOWER LOBES	0	NO TARGET DETECTED	SPUTUM	-
15	1523677	INFECTIVE, LEFT PNEUMOTHORAX, S/C EMPHYSEMA	4	K.PNEUMONIA 107, E.COLI104 , INFLUENZAE B	ET SECRETION	NDM, CTX-M, OXA-48 LIKE, VIM, KPC
16	1004498	ORGANISING PHASE OF PNEUMONIAE	5	ACINETOBACTER 107, K. PNEUMONIA 105	ET SECRETION	NDM, CTX-M, OXA-48 LIKE, VIM
17	1526330	ACUTE LUNG INJURY ?VIRAL PNEUMONIAE	1	P.AERUGINOSA 107, STAPH. AUREUS 107, ADENOVIRUS	SPUTUM	NDM, VIM, IMP, MREJ, mecA/C
18	1530207	B/L MILD PE, COLLPASE AND CONSOLIDATION AND SEPTAL THICKENING B/L UPPER LOBES	15	K.PNEUMONIA 104	ET SECRETION	NDM, IMP, VIM, CTX-M, OXA-48 LIKE
19	993180	-	1	P.AERUGINOSA 104, HUMAN RHINOVIRUS/ENTEROVIRUS	SPUTUM	IMP, NDM, VIM
20	1153694	CONSOLIDATION IN B/L LUNGS WITH MULTIPLE AIR SPACE NODULES	1	NO TARGET DETECTED	SPUTUM	-
21	1477587	-	2	HUMAN RHINOVIRUS/ENTEROVIRUS	SPUTUM	-
22	1481656	INFECTIVE VIRAL PNEUMONIA-PATCHY CONSOLIDATION WITH GGO	4	INFLUENZAE B	SPUTUM	-
23	1486636	-	2	H.INFLUENZAE 106, CORONAVIRUS, ENTEROBACTER CLOACAE 104	SPUTUM	NDM, VIM
24	30484	FIBROBRONCHIECTATIC CHANGES B/L LUNGS WITH LARGE CONFLUENT AREA OF GGOS	5	K. PENUMONIAE 104, STREPT AGALACTIAE 104	SPUTUM	IMP, NDM, CTX-M, OXA-48 LIKE
25	1442527	PATCHY AREAS OF AIR SPACE OPACIFICATION IN LEFT LUNG WITH MILD PE	2	NO TARGET DETECTED	SPUTUM	-
26	872071	PATCHY AREAS OF CONSOLIDATION WITH SURROUNDING GGOS	3	ACINETOBACTER 107, SERRATIA 105, STAPH AERUS 104, ENTEROBACTER 104	SPUTUM	IMP, VIM
27	1455152	B/L CENTRILOBULAR NODULES WITH BRONCHIAL DILATATION	1	ENTEROBACTER 105, H. INFLUENZAE 104, K. PNEUMONIA 104, STREP AGALACTIAE 104, INFLUENZAE B	SPUTUM	IMP, VIM, NDM, OXA-48 LIKE
28	1436051	EXTENSIVE GGOS WITH SEPTAL THICKENING B/L LUNGS, MILD B/L PE	9	ADENOVIRUS	SPUTUM	-
29	1542327	EXTENSIVE CONSFLUENT AREAS OF GG HAZE IN B/L LUNGS	2	ADENOVIRUS	ET SECRETION	-
30	1468887	LEFT LL PNEUMONIA	9	K.PNEUMONIA 106	SPUTUM	CTX-M, NDM, IMP, OXA-48 LIKE
31	1596894	INFECTIVE- VIRAL PNEUMONIA	2	K.PNEUMONIA 104, PSEUDOMONAS 104, INFLUENZAE A	ET SECRETION	IMP, NDM, OXA-48 LIKE, VIM
32	1640035	CONSOLIDATION, DIFFUSE GROUND GLASS OPACIFICATION	3	STAPH. AUREUS 107, PARAINFLUENZAE VIRUS	ET SECRETION	mecA/C, MREJ
33	1642389	ARDS	4	INFLUENZAE A, H1N1	ET SECRETION	-
34	859282	ILD, CONSOLIDATION LEFT UPPER LOBE	9	ACINETOBACTER BAUMANNI 107, E. COLI 104	ET SECRETION	-
35	1623259	MILD B/L PE AND PERICARDIAL EFFUSION	11	E. COLI 104, PSEUDOMONAS 104, STEPT AGALACTIAE 104	SPUTUM	NDM, IMP, VIM, CTX-M, OXA-48 LIKE
36	204048	MULTIPLE PATCHY AREAS OF CONSOLIDATION B/L LUNGS	1	ACINETOBACTER 107, P. AERUGINOSA 104, E.COLI 104, K. PENUMONIA 104	SPUTUM	NDM, CTX-M, OXA-48 LIKE
37	1647164	-	3	ACINETOBACTER 107, K. PNEUMONIA 106, E.COLI 105, INFLUENZAE A	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
38	1541629	RETICULATIONS WITH GROUND GLASS HAZE, LEFT PE	5	ACINETOBACTER 107, P. AERUGINOSA 105	ET SECRETION	NDM
39	1595646	ATYPICAL INFECTION, ARDS	1	STREP. PNEUMONIA 106	ET SECRETION	-
40	1476947	-	0	H. INLUENZAE 106, CORONAVIRUS	SPUTUM	-
41	1549153	-	5	NO TARGET DETECTED	ET SECRETION	-
42	1643768	-	1	K. PENUMONIAE 107, PROTEUS MIRABILIS 107, ACINETOBACTER 105, E.COLI 104, RSV	ET SECRETION	NDM, CTX-M, OXA-48 LIKE, VIM
43	104545	AREAS OF CONSOLIDATION WITH GGOS IN B/L LUNGS	6	HUMAN RHINOVIRUS/ENTEROVIRUS	ET SECRETION	-
44	696374	B/L DIFFUSE LUNG INJURY WITH PE ? INFECTIVE	7	ACINETOBACTER 107, INFLUENZAE A	ET SECRETION	NDM, CTX-M, VIM
45	1600035	DIFFUSE GGOS IN B/L LUNGS	6	STAPH AERUES 104	SPUTUM	mecA/C, MREJ
46	1614830	-	3	STAPH AERUES 104	ET SECRETION	-
47	1599887	-	3	K. PNEUMONIA 107, ACINETOBACTER 107	ET SECRETION	NDM, OXA-48 LIKE, VIM
48	1470586	-	1	INFLUENZA B	SPUTUM	-
49	57301	-	2	ACINETOBACTER 104	SPUTUM	NDM
50	1447506	-	1	PARAINFLUENZA	ET SECRETION	-
51	1410992	-	1	HUMAN METAPNEUMOVIRUS	SPUTUM	-
52	1470426	-	1	ACINETOBACTER BAUMANNI 106	ET SECRETION	CTX-M, NDM, VIM
53	1473465	EXTENSIVE AREAS OF CONSOLIDATION, CAVITATORY PNEUMONIA	2	INFLUENZAE B	ET SECRETION	-
54	1287339	EXTENSIVE CENTRILOBULAR NODULES IN B/L LUNGS	1	ACINETOBACTER BAUMANNI 107, P.AERUGINOSA 105, E.COLI 104, PARAINFLUENZAE	ET SECRETION	IMP, NDM, CTX-M, OXA-48 LIKE
55	1332477	B/L CONFLUENT GGOS, CONSOLIDATIONS	5	K. PENUMONIA 104, HUMAN RHINOVIRUS/ENTEROVIRUS	SPUTUM	NDM, CTX-M, OXA-48 LIKE, VIM
56	1485302	B/L EXTENSIVE CONSOLIDATIONS	1	H.INFLUENZAE 106, CORONAVIRUS, HUMAN RHINOVIRUS	ET SECRETION	-
57	1355061	-	11	ACINETOBACTER 107	ET SECRETION	NDM
58	1391288	ATYPICAL INFECTION	1	INFLUENZAE A	ET SECRETION	-
59	1374014	AREAS OF PARENCHYMAL OPACIFICATION, GROUND GLASS HAZE	30	INFLUENZAE A	ET SECRETION	-
60	398237	-	18	RSV	SPUTUM	-
61	1416415	-	8	K. PNEUMONIA 107, ACINETOBACTER 104, INFLUENZAE A	SPUTUM	NDM, CTX-M, OXA-48 LIKE
62	1421117	-	0	E. COLI 107, ACINETOBACTER 107	ET SECRETION	NDM, CTX-M
63	1426846	GGO, ATYPICAL INFECTION	11	NO TARGET DETECTED	ET SECRETION	-
64	1126755	BIBASILAR RETICULATIONS	27	ACINETOBACTER 106, K. PNEUMONIA 105	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
65	1355780	B/L PATCHY GGOS-INFECTIVE, VIRAL	3	ACINETOBACTE 107, K. PNEUMONIA 106, E.COLI 104, ENTEROBACTER 104, INFLUENZAE A	SPUTUM	NDM, CTX-M, OXA-48 LIKE, VIM
66	1355790	ARDS WITH B/L PLEURAL EFFUSION	8	P. AERUGINOSA 105	ET SECRETION	NDM
67	1347160	-	1	NO TARGET DETECTED	ET SECRETION	-
68	56623	-	6	K. PNEUMONIA 107	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
69	1416294	B/L PLEURAL EFFUSION	21	ACINETOBACTER 105, E.COLI 104, HUMAN RHINOVIRUS, ENTEROVIRUS	ET SECRETION	NDM

		ROBIOLOGY			
Sr No	MRD	GRAM STAIN	CULTURE	CULTURE SENSITIVITY	EMPIRICAL ANTIBIOTIC
1	1453273	PUS CELLS	ACINETOBACTER 103	COLISTIN	MEROPENEM, TEICOPLANIN
2	1473509	GPC, SEPTATE HYPHAE	E.COLI 104	COLISTIN, AMIKACIN, GENTAMICIN, TIGECYCLINE	PIPERACILLIN TAZOBACTAM, TEICOPLANIN, AZITHROMYCIN
3	1390373	GPC,GNB,GPB,BUDDING YEAST	K.PNEUMONIAE 105	COLISTIN, AMIKACIN, GENTAMICIN	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, CASPOFUNGIN
4	1471395	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, TRIMETHOPRIME-SULFAMETOXAZOLE, CASPOFUNGIN
5	957093	BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, TAMIFLU, VORICONAZOLE
6	1442804	GNCB,BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, VORICONAZOLE
7	1448452	NO GROWTH	K.PNEUMONIAE 104	AMIKACIN	MEROPENEM, TEICOPLANIN, TIGECYCLINE, VORICONAZOLE
8	1445555	GNB,BUDDING YEAST LIKE CELLS	ACINETOBACTER 104, E.COLI 103	COLISTIN, AMIKACIN, MINOCYCLINE	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
9	1478579	NO GROWTH	K.PNEUMONIAE 104	COLISTIN, AMIKACIN, TIGECYCLINE	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
10	1495206	BUDDING YEAST LIKE CELLS	NO GROWTH	-	MEROPENEM, TEICOPLANIN
11	1418303	GNCB	K. PNEUMONIA 105, ACINETOBACTER 103	COLISTIN	MEROPENEM, TEICOPLANIN
12	1472301	NO GROWTH	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, TEICOPLANIN
13	264953	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
14	1324791	GPC,GPB,GNCB,BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
15	1523677	HYALINE SEPTATE FUNGAL HYPHAE	NO GROWTH	-	MEROPENEM, CLINDAMYCIN, COLISTIN, VORICONAZOLE
16	1004498	GNCB,BUDDING YEAST LIKE CELLS	ACINETOBACTER 103	COLISTIN, MINOCYCLINE	MEROPENEM, TEICOPLANIN, FLUCONAZOLE
17	1526330	GPC, GNB, GNCB, BUDDING YEAST, PSEUDOHYPHAE	P. AERUGINOSA 102	COLISTIN	PIPERACILLIN, TAZOBACTAM, TEICOPLANIN
18	1530207	GPC, GNB, GPB	K.PNEUMONIAE 105	COLISTIN, AMIKACIN, GENTAMICIN, TIGECYCLINE, DOXYCYCLINE	MEROPENEM, TEICOPLANIN
19	993180	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN
20	1153694	GPC, BUDDING YEAST LIKE CELLS	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, VORICONAZOLE
21	1477587	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN
22	1481656	GNB, GNCB, BUDDING YEAST WITH PSEUDOHYPHAE	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
23	1486636	GPC, GNCB	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN, TAMIFLU
24	30484	GPC, GPB	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
25	1442527	GNB, GNCB, BUDDING YEAST LIKE AND PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN
26	872071	GNB, GNCB	ACINETOBACTER 104	COLISTIN, CEFOPERAZONE, SULBACTAM, MINOCYCLINE, CEFIPIME	MEROPENEM, TEICOPLANIN
27	1455152	GPC, GNB, GNCB	NO GROWTH	-	CEFTRIAXONE, CLARITHROMYCIN, PIPERACILLIN, TAZOBACTAM
28	1436051	GPC	NO GROWTH	-	CEFTRIAXONE, FLUCONAZOLE
29	1542327	GNCB, BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, DOXYCYCLINE, CEFTRIAXONE
30	1468887	GPC, BUDDING YEAST LIKE CELLS	NO GROWTH	-	CEFTRIAXONE, TEICOPLANIN
31	1596894	GPC	K. PNEUMONIA 102	COLISTIN, TIGECYCLINE, DOXYCYCLINE, TETRACYCLINE	MEROPENEM, TEICOPLANIN
32	1640035	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, DOXYCYCLINE
33	1642389	NO GROWTH	NO GROWTH	-	IMIPENEM, TEICOPLANIN
34	859282	BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	AMOXICILLIN, CLAVULUNIC ACID
35	1623259	NO GROWTH	NO GROWTH	-	CEFTRIAXONE, DOXYCYCLINE
36	204048	GPC	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
37	1647164	GPC, GNB, GNCB	NO GROWTH	-	CEFTRIAXONE, SULBACTAM, AZITHROMYCIN
38	1541629	GPC, BUDDING YEAST, PSEUDOHYPHAE	ACINETOBACTER 105	COLISTIN	PIPERACILLIN, TAZOBACTAM, CLARITHROMYCIN
39	1595646	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, VORICONAZOLE, COLISTIN
40	1476947	GPC, GPB, BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
41	1549153	BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	COLISTIN, MEROPENEM, TEICOPLANIN, VORICONAZOLE
42	1643768	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, TAMIFLU
43	104545	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
44	696374	GPC, GNB, BUDDING YEAST, PSEUDOHYPHAE	CITROBACTER KOSERI	AMOXYCILLIN, CLAVULUNIC ACID	MEROPENEM, TIGECYCLINE, VORICONAZOLE
45	1600035	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, DOXYCYCLINE
46	1614830	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
47	1599887	GPC, PUS CELL	NO GROWTH	-	MEROPENEM, TEICOPLANIN
48	1470586	GPC, GNB, BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	PIPERACILLIN, AZITHROMYCIN, TAMIFLU
49	57301	GPC, GNCB, BUDDING YEAST	NO GROWTH	-	CEFOPERAZONE, SULBACTAM
50	1447506	NO GROWTH	NO GROWTH	-	PIPERACCILIN, TAZOBACTAM AZITHROMYCIN, TAMIFLU
51	1410992	GPC, GNB, GPB	NO GROWTH	-	PIPERACILLIN+TAZOBACTEM, AZITHROMYCIN, TEICOPLANIN
52	1470426	GNCB	ACINETOBACTER 105	COLISTIN	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
53	1473465	GPC, BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
54	1287339	GNCB	ACINETOBACTER 105	COLISTIN	MEROPENEM, TARGOCID
55	1332477	GPC, GNB, BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, TRIMETHOPRIME-SULFAMETHOXAZOLE
56	1485302	GPC, GNB	NO GROWTH	-	CEFOPERAZONE, SULBACTAM, TEICOPLANIN, METRONIDAZOLE
57	1355061	GNB, BUDDING YEAST, PSEUDOHYPHAE	K. PNEUMONIA 105, ACINETOBACTER 103	COLISTIN, AMIKACIN, CEFTAZIDIME, AVIBACTAM	CEFTRIAXONE, TEICOPLANIN
58	1391288	GNB	K. PNEUMONIA 103	COLISTIN, AMIKACIN, GENTAMICIN	MEROPENEM, TEICOPLANIN
59	1374014	NO GROWTH	STENOTROPHOMONAS MALTOPHILIA 103	LEVOFLOXACIN, MINOCYCLINE	PIPERACILLIN TAZOBACTAM, TEICOPLANIN
60	398237	GPC, GNCB, BUDDING YEAST, PSEUDOHYPHAE	ACINETOBACTER 103, E. COLI 103	COLISTIN, MINOCYCLINE	MEROPENEM, TEICOPLANIN
61	1416415	GPC	K. PNEUMONIA 102	COLISTIN, AMIKACIN, IMIPENEM	MEROPENEM, TEICOPLANIN, METRONIDAZOLE
62	1421117	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN
63	1426846	GPC	NO GROWTH	-	IMIPENEM, TEICOPLANIN, AZITHROMYCIN, TRIMETHOPRIME-SULFAMETHOXAZOLE, VORICONAZOLE
64	1126755	GNB	K. PNEUMONIA 103	COLISTIN, AMIKACIN	MEROPENEM, TEICOPLANIN
65	1355780	GNCB	ACINETOBACTER 104	COLISTIN, MINOCYCLINE	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
66	1355790	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
67	1347160	BUDDING YEAST, PSEUDOHYPHAE	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
68	56623	NO GROWTH	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, TEICOPLANIN
69	1416294	GPC, GNCB	ACINETOBACTER 103, STAPH HOMINIS 103	COLISTIN, COTRIMOXAZOLE, TEICOPLANIN, GENTAMICIN	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, VORICONAZOLE

	TREATMENT			OUTCOME		
Sr No	MRD	DAYS AFTER WHICH ANTIBIOTIC CHANGED	ANTIBIOTICS REVISED AFTER FILMARRAY REPORT	CLINICAL	DAYS OF ICU STAY	RADIOLOGICAL
1	1453273	7	COLISTIN,MEROPENEM,TEICOPLANIN, LEVOFLOXACIN	POST EXTUBATION, ASYMPTOMATIC	25	CXR-CLEAR
2	1473509	3	COLISTIN, IMIPENEM, CASPOFUNGIN	DISCHARGED ON OXYGEN SUPPORT	12	DIFFUSE OPACITIES
3	1390373	7	CEFTAZIDIME, AVIBACTAM, COLISTIN,CLINDAMYCIN, VORICONAZOLE,CASPOFUNGIN	INTUBATED	9	RIGHT LUNG COLLAPSE
4	1471395	12	CEFTAZIDIME, AVIBACTAM, POLY-B,AZTREONAM,TEICOPLANIN,CASPOFUNGIN	INTUBATED	18	B/L MULTIPLE OPACITIES
5	957093	-	NOT CHANGED	OFF OXYGEN	5	CONSOLIDATION LEFT LUNG
6	1442804	4	POLY B,VANCOMYCIN, LEVOFLOXACIN, MINOCYCLIN, CASPOFUNGIN	DISCHARGED ON NIV	7	WORSENED,B/L PLEURAL EFFUSION
7	1448452	10	CEFTAZIDIME, AVIBACTAM, COLISTIN, TIGECYCLINE	INTUBATED	17	B/L PLEURAL EFFUSION
8	1445555	7	IMIPENEM,TIGECYCLINE	INTUBATED	15	RIGHT CP ANGLE BLUNT
9	1478579	8	CEFTAZIDIME, AVIBACTAM, RIBAVIRIN, VORICONAZOLE	ON NRBM+VENTURI INTEMITTENT	35	RESOLUTION OF EFFUSION
10	1495206	9	CEFTAZIDIME, AVIBACTAM,POLY B, VANCOMYCIN	EXTUBATED,ON RA	9	SMALL CONSOLIDATION LEFT UL
11	1418303	1	CEFTAZIDIME, AVIBACTAM,MEROPENEM, COLISTIN	EXTUBATED, TRACHEOSTOMY INSITU	5	LEFT LUNG PATCH
12	1472301	2	MEROPENEM, TEICOPLANIN, LEVOFLOXACIN	NIV SUPPORT TO ROOM AIR	0	CLEAR
13	264953	8	POLY B, TIGECYCLINE	INTUBATED	11	DIFFUSE OPACITIES
14	1324791	-	NOT CHANGED	PCD OUT,OFF OXYGEN	0	MINIMAL LEFT PLEURAL EFFUSION
15	1523677	4	COLISTIN, CEFTAZIDIME, AVIBACTAM, AZTREONAM, TIGECYCLINE, CASPOFUNGIN	EXTUBATED, ICD OUT	7	PNEUMOTHORAX RESOLVED
16	1004498	11	COLISTIN, MEROPENEM, TEICOPLANIN, FLUCONAZOLE	INTUBATED, EXPIRED	16	LEFT GROSS PE, RIGHT LUNG COLLAPSE
17	1526330	-	NOT CHANGED	COUGH IMPROVED, ON BINASAL SUPPORT @2L/MIN	4	IMPROVED, MINIMAL OPACITIES
18	1530207	8	CEFTAZIDIME,AVIBACTAM, TIGECYCLINE, COLISTIN, AZTREONAM, ANIDULAFUNGIN	WORSENING OF SOB, INTUBATED	15	RIGHT SIDED PE, MULTIPLE PATCHES
19	993180	2	COLISTIN, TEICOPLANIN, CEFTAZIDIME, AVIBACTAM	SOB WORSENED, ON NIV SUPPORT TRIPLE PORT	11	RIGHT MASSIVE PELURAL EFFUSION
20	1153694	-	NOT CHANGED	FEVER RESOLVED, ON RA	3	CLEAR
21	1477587	-	NOT CHANGED	OFF OXYGEN	1	CLEAR
22	1481656	3	PIPERACILLIN, TAZOBACTAM, TAMIFLU	OFF OXYGEN	0	RIGHT SIDE SMALL PATCH LEFT
23	1486636	-	NOT CHANGED	OFF OXYGEN	6	CLEAR
24	30484	7	MEROPENEM, TEICOPLANIN, TIGECYCLINE,DOXYCYCLINE, FLUCONAZOLE	INTERMITTENT NIV WITHOUT OXYGEN	8	B/L PATCHES LEFT
25	1442527	-	NOT CHANGED	OFF OXYGEN, SYMPTOMS RESOLVED	2	CLEAR
26	872071	-	NOT CHANGED	SYMPTOMS RESOLVED	4	CLEAR
27	1455152	1	TEICOPLANIN, CLARITHROMYCIN, TAMIFLU, MEROPENEM	OFF OXYGEN	0	CLEAR
28	1436051	11	CEFTAZIDIME, AVIBACTAM, TIGECYCLINE, POSACONAZOLE	INTUBATED	16	WORSENED, LEFT LUNG COLLAPSE
29	1542327	8	MEROPENEM, TEICOPLANIN, CEFTAZIDIME, AVIBACTAM, COLISTIN, ANIDULAFUNGIN, LEVOFLOXACIN	EXTUBATED, OFF OXYGEN	29	CLEAR
30	1468887	9	CEFTAZIDIME, AVIBACTAM, COLISTIN, TEICOPLANIN	OFF OXYGEN	12	CLEAR
31	1596894	1	MEROPENEM, TEICOPLANIN, DOXYCYCLINE, TAMIFLU	INTUBATED, EXPIRED	5	ARDS
32	1640035	8	MEROPENEM, TEICOPLANIN, DOXYCYCLINE, LINEZOLID, GENTAMICIN	EXTUBATED	14	CLEAR
33	1642389	1	IMIPENEM, TEICOPLANIN, LEVOFLOXACIN, TAMIFLU	NIV SUPPORT	15	ARDS
34	859282	9	COLISTIN, TEICOPLANIN	EXTUBATED, ROOM AIR	12	CLEAR
35	1623259	5	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, ATT	OFF OXYGEN	0	MINIMAL B/L PLEURAL EFFUSION
36	204048	1	CEFTAZIDIME, AVIBACTAM, COLISTIN, TIGECYCLINE	INTUBATED	17	ARDS
37	1647164	-	NOT CHANGED	EXTUBATED, OFF OXYGEN	6	CLEAR
38	1541629	3	MEROPENEM, TEICOPLANIN, METRONIDAZOLE, DOXYCYCLINE, TAMIFLU, POLY B	INTUBATED	12	ARDS
39	1595646	5	CEFTRIAXONE, SULBACTAM, COLISTIN, VORICONAZOLE	EXTUBATED, OFF OXYGEN	15	HAZINESS LEFT LUNG BASE
40	1476947	-	NOT CHANGED	DOMICILLIARY NIV	0	CLEAR
41	1549153	7	CEFTAZIDIME, AVIBACTAM, AZTREONAM, COLISTIN, TEICOPLANIN	INTUBATED, EXPIRED	20	ARDS
42	1643768	1	CEFTAZIDIME, AVIBACTAM, COLISTIN	INTUBATED, EXPIRED	8	ARDS
43	104545	-	NOT CHANGED	INTUBATED, EXPIRED	8	ARDS
44	696374	7	MEROPENEM, TEICOPLANIN, VORICONAZOLE, COLISTIN	INTUBATDE, CRRT	7	ARDS
45	1600035	8	MEROPENEM, TEICOPLANIN, DOXYCYCLINE, COLISTIN, CLINDAMYCIN	INTUBATED	25	ARDS
46	1614830	-	NOT CHANGED	INTUBATED, EXPIRED	9	ARDS
47	1599887	1	COLISTIN, TEICOPLANIN, CLINDAMYCIN, METRONIDAZOLE, CASPOFUNGIN	INTUBATED	1	ARDS
48	1470586	-	NOT CHANGED	SYMPTOMS RESOLVED	1	CLEAR
49	57301	-	NOT CHANGED	OFF OXYGEN	7	CLEAR
50	1447506	-	NOT CHANGED	EXTUBATED, OFF OXYGEN	1	CLEAR
51	1410992	1	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN, TAMIFLU, VORICONAZOLE	INTUBATED	6	LEFT PLEURAL EFFUSION, CONSOLIDATIONS B/L
52	1470426	1	MEROPENEM, TEICOPLANIN, SULBACTAM, POLY B	INTUBATED, INOTROPES	14	ARDS
53	1473465	-	NOT CHANGED	INTUBATED	11	B/L CONSOLIDATIONS
54	1287339	-	NOT CHANGED	OFF OXYGEN	4	CLEAR
55	1332477	6	COLISTIN, CEFTAZIDIME, AVIBACTAM, CLINDAMYCIN	INTUBATED, INOTROPES	42	B/L EXTENSIVE CONSOLIDATIONS
56	1485302	1	CEFOPERAZONE, SULBACTAM, COLISTIN, TEICOPLANIN, METRONIDAZOLE	INTUBATED, INOTROPES	15	ARDS
57	1355061	11	CEFTAZIDIME, AVIBACTAM, COLISTIN, TEICOPLANIN, CEFTRIAXONE, METRONIDAZOLE	INTUBATED	8	B/L CONSOLIDATIONS
58	1391288	1	MEROPENEM, TEICOPLANIN, VORICONAZOLE, TAMIFLU	POST TRACHEOSTOMY, ON VENTILATOR	22	ARDS
59	1374014	2	COLISTIN, PIPERACILLIN TAZOBACTAM, CASPOFUNGIN	POST TRACHEOSTOMY, ON VENTILATOR	40	B/L CONSOLIDATIONS
60	398237	5	MEROPENEM, COLISTIN, TIGECYCLIN, VORICONAZOLE	INTUBATED, INOTROPES	42	B/L CONSOLIDATIONS
61	1416415	1	COLISTIN, MEROPENEM, TEICOPLANIN, METRONIDAZOLE, LEVOFLOXACIN, LIPOSOMAL AMP B	INTUBATED	2	B/L PLEURAL EFFUSION
62	1421117	1	MEROPENEM, TEICOPLANIN, POLY B, CASPOFUNGIN	INTUBATED, INOTROPES	21	LEFT LUNG COLLAPSE
63	1426846	5	CEFTAZIDIME, AVIBACTAM, CLINDAMYCIN, TRIMETHOPRIME-SULFAMETHOXAZOLE	POST TRACHEOSTOMY, ON VENTILATOR	31	B/L PLEURAL EFFUSION
64	1126755	20	CEFTAZIDIME, AVIBACTAM, COLISTIN, TEICOPLANIN	POST TRACHEOSTOMY, ON VENTILATOR	44	B/L CONSOLIDATIONS
65	1355780	3	MEROPENEM, TEICOPLANIN, CEFTAZIDIME, AVIBACTAM, COLISTIN	POST EXTUBATION	7	B/L MINIMAL PLEURAL EFFUSION
66	1355790	9	MEROPENEM, TEICOPLANIN, COLISTIN	ECMO, INTUBATED, SHOCK	16	ARDS
67	1347160	1	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, TAMIFLU, VORICONAZOLE	INTUBATED	4	B/L CONSOLIDATIONS
68	56623	6	MEROPENEM, TEICOPLANIN, CEFTAZIDIME, AVIBACTAM, AZTREONAM	INTUBATED, SHOCK	13	B.L PLEURAL EFFUSION
69	1416294	13	CEFTAZIDIME, AVIBACTAM, COLISTIN, METRONIDAZOLE, VORICONAZOLE	INTUBATED, ICD INSITU	36	B/L CONSOLIDATIONS, LEFT PELURAL EFFUSION

				ADDITIONAL INFORMATION			Visitation Details			EXAMINATION FINDINGS	
Sr No	MRD	Age(YRS)	Gender	COMPLAINS	COMORBIDITIES	SATURATION	ADMISSION DATE	DATE OF DISCHARGE	Result	AUSCULTATION	CXR
70	1413661	58	M	FEVER, PRODUCTIVE COUGH, DYSPNEA	SARCOIDOSIS	84% ON RA	03/11/22	09/12/22	DAMA	RIGHT SIDE CREPTS	RIGHT UPPER LOBE CONSOLIDATION
71	1395251	33	M	DYSPNEA	NO COMORBIDITY	80% ON RA	10/10/22	18/10/22	EXPIRED	DECREASED AE LEFT SIDE	LEFT SIDE HAZINESS
72	1386420	55	M	FEVER, DYSPNEA	COPD	82% ON RA	24/09/22	30/09/22	EXPIRED	B/L CREPTS	B/L LOWER LOBE CONSOLIDATION
73	1388447	56	M	FEVER, PRODUCTIVE COUGH	DM, CKD	88% ON RA	28/09/22	04/10/22	EXPIRED	B/L AIR ENTRY DECREASED	B/L LOWER ZONE HAZE
74	1370920	45	M	FEVER, DYSPNEA, PRODUCTIVE COUGH	HTN	92% ON RA	31/08/22	16/09/22	EXPIRED	B/L CREPTS	B/L HAZINESS
75	1498019	46	M	DYSPNEA	DM, CKD	81% ON RA	12/04/23	02/05/23	DISCHARGE	RIGHT AIR ENTRY DECREASED	RIGHT MIDDLE LOBE CONSOLIDATION
76	1483103	46	M	DYSPNEA, FEVER	NO COMORBIDITY	GASPING	18/03/23	18/03/23	EXPIRED	B/L AIR ENTRY DECREASED	B/L HAZINESS
77	1438579	29	F	FEVER, DYSPNEA, COUGH	NO COMORBIDITY	92% ON RA	28/12/22	21/01/23	DAMA	LEFT SIDE AIR ENTRY DECREASED	LEFT SIDE HAZINESS
78	1441890	21	M	DYSPNEA	NO COMORBIDITY	GASPING	05/01/23	15/01/23	EXPIRED	RIGHT AIR ENTRY DECREASED	RIDE SIDE CONSOLIDATIONS
79	1436022	69	F	FEVER, PRODUCTIVE COUGH	DM, HTN, CAD	84% ON RA	22/12/22	21/01/23	EXPIRED	B/L CREPTS	LEFT SIDE HAZINESS
80	1445305	39	F	FEVER, PRODUCTIVE COUGH, DYSPNEA	NO COMORBIDITY	90% ON RA	13/01/23	15/02/23	DISCHARGE	RIGHT AIR ENTRY DECREASED	RIGHT MIDDLE LOBE CONSOLIDATION
81	1449720	72	F	DYSPNEA	DM, CAD POST PTCA	GASPING	21/01/23	22/01/23	EXPIRED	LEFT AIR ENTRY ABSENT	LEFT PLEURAL EFFUSION
82	1467394	76	M	FEVER, COUGH	HTN, COPD	86% ON RA	21/02/23	10/03/23	DISCHARGE	B/L CREPTS	B/L CONSOLIDATION
83	1471137	81	M	PRODUCTIVE COUGH, DYSPNEA	COPD, OLD PULMONARY KOCHS	88%ON RA	27/02/23	21/03/23	EXPIRED	B/L CREPTS	RIGHT MIDDLE LOBE HAZINESS

Sr No	IMAGING		DAYS AFTER WHICH FILM ARRAY WAS DONE	MIC		
	MRD	CT CHEST		FILM ARRAY	SAMPLE USED	RESISTANCE GENE
70	1413661	B/L PLEURAL EFFUSION	4	ACINETOBACTER 107, HUMAN RHINOVIRUS, ENTEROVIRUS	ET SECRETION	NDM, VIM
71	1395251	-	4	H. INFLUENZAE 104, STAPH AEUREUS 104	ET SECRETION	-
72	1386420	-	6	K. PNEUMONIA 104, ACINETOBACTER 104, INFLUENZA A	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
73	1388447	BASAL CONSOLIDATION WITH INFECTIOUS BRONCHIOLITIS	7	STREP AGALACTIAE 105, STREP PNEUMONIA 104, INFLUENZAE A	ET SECRETION	-
74	1370920	-	3	ACINETOBACTER 107, K. PNEUMONIA 105	ET SECRETION	NDM, CTX-M, OXA-48 LIKE
75	1498019	FUNGAL ETIOLOGY	4	NO TARGET DETECTED	BAL	-
76	1483103	ARDS	0	STREP PNEUMONIAE	ET SECRETION	-
77	1438579	FOCAL ALVEOLITIS LEFT LUNG	5	ACINETOBACTER 107, STAPH AERUES 105, K. PNEUMONIAE 104	ET SECRETION	NDM, CTX-M, OXA-48 LIKE, mecA/C, MREJ
78	1441890	B/L CONSOLIDATIONS WITH GGOS	6	P. AERUGINOSA 107	ET SECRETION	NDM, CTX-M
79	1436022	INFECTIVE ETIOLOGY VIRAL	19	INFLUENZAE A	ET SECRETION	-
80	1445305	EXTENSIVE AREAS OF GROUND GLASS HAZE AND CONSOLIDATION B/L LUNGS	3	ACINETOBACTER 106, INFLUENZAE B	ET SECRETION	NDM, IMP, CTX-M, VIM
81	1449720	-	1	H. INFLUENZAE 107, INFLUENZAE A	ET SECRETION	-
82	1467394	INFECTIVE ETIOLOGY IN ORGANISING PHASE B/L LUNGS	2	HUMAN RHINOVIRUS/ENTEROVIRUS	SPUTUM	-
83	1471137	INFECTIVE ALVEOLITIS	1	K. PNEUMONIAE 107, ACINETOBACTER 104, H.INFLUENZAE 104, RSV	ET SECRETION	NDM, CTX-M, OXA-48 LIKE

Sr No	MRD	GRAM STAIN	CULTURE	CULTURE SENSITIVITY	EMPIRICAL ANTIBIOTIC
70	1413661	GNCB	ACINETOBACTER 105	COLISTIN, MINOCYCLINE	MEROPENEM, TEICOPLANIN, METRONIDAZOLE
71	1395251	BUDDING YEAST AND PSEUDOHYPHAE	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
72	1386420	NO GROWTH	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
73	1388447	NO GROWTH	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
74	1370920	GNCB, BUDDING YEAST	K. PNEUMONIA 105	COLISTIN, AMIKACIN	PIPERACILLIN, TAZOBACTAM, TEICOPLANIN
75	1498019	GPC, BUDDING YEAST AND PSEUDOHYPHAE	NO GROWTH	-	CEFTRIAXONE, AZITHROMYCIN
76	1483103	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
77	1438579	GPC, GNCB	STAPH HOMINIS, ACINETOBACTER 105	COLISTIN, COTRIMOXAZOLE, TEICOPLANIN, GENTAMICIN	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
78	1441890	GNB	P. AERUGINOSA 105	COLISTIN	MEROEPENEM, TEICOPLANIN, METRONIDAZOLE
79	1436022	NO GROWTH	NO GROWTH	-	PIPERACILLIN, TAZOBACTAM, AZITHROMYCIN
80	1445305	NO GROWTH	ACINTOBACTER 104	COLISTIN	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, VORICONAZOLE
81	1449720	GPC	NO GROWTH	-	MEROPENEM, TEICOPLANIN, METRONIDAZOLE, VANCOMYCIN
82	1467394	NO GROWTH	NO GROWTH	-	MEROPENEM, TEICOPLANIN, AZITHROMYCIN
83	1471137	GPC, GNB, BUDDING YEAST, PSEUDOHYPHAE	K. PNEUMONAE 103	COLISTIN, AMIKACIN, TIGECYCLINE	MEROPENEM, TEICOPLANIN, VORICONAZOLE

	TREATMENT			OUTCOME		
Sr No	MRD	DAYS AFTER WHICH ANTIBIOTIC CHANGED	ANTIBIOTICS REVISED AFTER FILMARRAY REPORT	CLINICAL	DAYS OF ICU STAY	RADIOLOGICAL
70	1413661	4	CEFTAZIDIME, AVIBACTAM, TEICOPLANIN, METRONIDAZOLE	INTUBATED	36	B/L CONSOLIDATIONS
71	1395251	4	MEROPENEM, TEICOPLANIN, COLISTIN, AZITHROMYCIN	INTUBATED	8	B/L HAZINESS
72	1386420	6	MEROPENEM, TEICOPLANIN, AZITHROMYCIN, TAMIFLU, VORICONAZOLE	INTUBATED, PERITONEAL DIALYSIS	7	ARDS
73	1388447	7	MEROPENEM, TEICOPLANIN, TAMIFLU	INTUBATED	7	B/L CONSOLIDATION
74	1370920	3	MEROPENEM, TEICOPLANIN, COLISTIN, AZITHROMYCIN	INTUBATED	17	ARDS
75	1498019	2	CEFTRIAXONE, AZITHROMYCIN, VORICONAZOLE	NIV SUPPORT	12	CLEAR
76	1483103	-	NOT CHANGED	INTUBATED, SHOCK	1	ARDS
77	1438579	6	MEROPENEM, VANCOMYCIN, ZAVICEFTA, AZTREONAM,COLISTIN	POST CRRT, INTUBATED	25	ARDS
78	1441890	5	MEROPENEM, TEICOPLANIN, COLISTIN, VORICONAZOLE	INTUBATED	11	B/L CONSOLIDATIONS
79	1436022	10	PIPERACILLIN, TAZOBACTAM, TAMIFLU	INTUBATED, SHOCK	28	B/L LOWER ZONE HAZINESS
80	1445305	3	MEROPENEM, TEICOPLANIN, COLISTIN, VORICONAZOLE, TAMIFLU	POST EXTUBATION	26	CLEAR
81	1449720	-	NOT CHANGED	INTUBATED	2	B/L PLEURAL EFFUSION
82	1467394	-	NOT CHANGED	NIV INTERMITTENT	10	B/L FIBROSIS
83	1471137	7	COLISTIN, ZAVICEFTA, AZTREONAM, TEICOPLANIN, TAMIFLU, VORICONAZOLE	INTUBATED, SHOCK	23	B/L CONSOLIDATION

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No. BFUHS/2K23p-TH/ 13293 Date 29/12/23

The Principal
Dayanand Medical College & Hospital
Ludhiana

Subject:: Approval of Plan of Thesis.

This is to inform you that the Faculty of Medical Sciences in its meeting held on 25.09.2023 has approved the plan of thesis of **Yuvika Saini**, a student of your college for **MD General Medicine** along with the names of Supervisor/Co-Supervisor as under:-

Topic Plan of Thesis
Role of multiplex pcr pneumonia panel in determining the diagnosis, antibiotics selection and outcome in patients with pneumonia .

Supervisor
Dr. Rajesh Mahajan
Professor
Dept. of Medicine

Co-Supervisor:-
Dr. Veenu Gupta
Prof. & Head
Dept. of Microbiology

Co-Supervisor:-
Dr. Akashdeep Singh
Prof. & Head
Dept. of Pulmonary Medicine

The student may submit the thesis in triplicate alongwith the plan in triplicate also, to the Controller of Examinations, BFUHS, Faridkot, at least six months before the commencement of theory examination, if he/she is otherwise eligible to take the examination. He /She may be directed to attach a photocopy of this letter with the forwarding letter while submitting thesis in the University along with the letter of approval of University for change of supervisor/Co-Supervisor, change of topic, if any.

Controller of Examinations

Note :

1. *If any discrepancy found regarding topic of thesis or Supervisor/Co-Supervisor, inform undersigned within one month after issue of this letter.*

ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA

THESIS PROPOSAL

FOR APPROVAL OF SUBJECT OF THESIS TO BE SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS

FOR THE DEGREE OF

MD

IN

GENERAL MEDICINE

OF THE

BABA FARID UNIVERSITY OF HEALTH SCIENCES

FARIDKOT

AUGUST, 2022

DR.YUVIKA SAINI

DEPARTMENT OF GENERAL MEDICINE
DAYANAND MEDICAL COLLEGE AND HOSPITAL
LUDHIANA

ABSTRACT OF PLAN OF THESIS

Title	ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA
For the degree of	MD General Medicine
Name of the candidate	Dr.Yuvika Saini
Supervisor	Dr. Rajesh Mahajan, Professor, Department of Medicine, DMCH, Ludhiana
Co-Supervisor	Dr. Veenu Gupta, Professor & Head, Department of Microbiology, DMCH, Ludhiana Dr. Akashdeep Singh, Professor & Head, Department of Pulmonary Medicine, DMCH, Ludhiana
Institution	Dayanand Medical College and Hospital, Ludhiana
University	Baba Farid University of Health Sciences, Faridkot

Introduction: Pneumonia is a common acute respiratory infection that affects the alveoli and distal airways; it is a major health problem and associated with high morbidity and short-term and long-term mortality in all age groups worldwide. Pneumonia is broadly divided into community-acquired pneumonia or hospital-acquired pneumonia.

Aims and Objectives: 1. To compare the clinical significance of diagnosing Pneumonia in patients with FilmArray versus those with standard methods. 2. To determine any difference in clinical cure of pneumonia between patients treated according to the FilmArray test's molecular results versus those treated with standard methods. 3. To determine whether there is an improvement in antimicrobial selection in participants treated according to the FilmArray test versus those treated with standard methods.

Materials and Methods: Cross-sectional study

1. Clinical Specimens. In ET secretions, BAL, sputum and blood cultures of hospitalized patients of DMCH Ludhiana.
2. Multiplex Real-Time PCR Assay. The specimens collected from ET secretions, BAL,Sputum.
3. Standard Methods- sputum for gram stain and culture sensitivity.
4. Cross-sectional study analysis.

Clinical significance: This will help reduce the duration of diagnosis aiding early diagnosis, tapering empirical antibiotics and starting specific antibiotics, reducing burden of unnecessary investigations, reducing burden on intestinal flora and decreasing antimicrobial resistance.

Keywords: Randomised controlled trial, Hospital-acquired pneumonia, Ventilator-associated pneumonia, medical outcomes, pneumonia hospital-acquired pneumonia; FilmArray; multiplexed BioFire Pneumonia Panel plus; genetic markers; antibiotic sensitivity.

(Signature) Candidate

(Signature) Co-supervisor

(Signature) Co-supervisor

(Signature) Supervisor

(Signature) Principal

CERTIFICATE OF FACILITIES AVAILABLE

This is to certify that the facilities for work on the subject of thesis titled **"ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA"** exist in the Department of General Medicine at Dayanand Medical College and Hospital, Ludhiana and will be provided to the candidate. We will see that the data being included in the thesis are genuine and is collected by the candidate herself under our supervision and guidance.

Supervisor

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Place : _____
Date : _____

APPROVAL PROFORMA
BY
RESEARCH & ETHICAL COMMITTEE
DAYANAND MEDICAL COLLEGE & HOSPITAL, LUDHIANA

Name of candidate	Dr Yuvika Saini
Department	General Medicine
Topic of Thesis	ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA
Likely date of appearing in PG examination	May/June , 2024
Date of enrollment	March 7, 2022
Name of Head of Department	Dr. Dinesh Gupta
1. Supervisor	Dr. Rajesh Mahajan
2. Co-Supervisor	Dr. Veenu Gupta Dr. Akashdeep Singh
Signature of Members of Research Committee with Stamp	**Signature of Members of Ethics Committee with Stamp**
Dr. Harpreet Kaur (Professor & Head, Pathology)	Mr. R K Sharma (Legal Expert)
Dr.J aspal Singh (Professor & Head, Surgery)	Dr. Ramit Mahajan (Associate Professor, Gastroenterology)
Dr. Dinesh Gupta (Professor & Head, Medicine)	Dr.Anu Sharma (Professor, Anatomy)
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Dr. Gurpreet S Wander (Vice Principal)	Dr. Gurpreet S Wander (Vice Principal & Professor & Head, Cardiology)
	Dr. Gagandeep Singh (Secretary, Ethics Committee Professor & Head, Neurology)

Approved: Yes / ~~No~~

Dr.Sandeep Puri
Chairperson
Research Committee

Chairperson
Research Committee

Approved: Yes / ~~No~~

Prof. Arvind Malhotra
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BABA FARID UNIVERSITY OF HEALTH SCIENCES, FARIDKOT

PROFORMA FOR REGISTRATION OF SUBJECT FOR DISSERTATION

1	NAME OF THE CANDIDATE AND ADDRESS	DR. YUVIKA SAINI VPO LAHRI GUJJRAN, TEH AND DIST PATHANKOT, PUNJAB
2	NAME OF THE INSTITUTE	DAYANAND MEDICAL COLLEGE AND HOSPITAL
3	COURSE OF STUDY AND SUBJECT	M.D. GENERAL MEDICINE
4	DATE OF ADMISSION OF COURSE	07/03/2022
5	TITLE OF THE TOPIC	ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA

6. BRIEF RESUME OF THE INTENDED WORK

6.1 NEED FOR THE STUDY

Pneumonia is a common acute respiratory infection that affects the alveoli and distal airways; it is a major health problem and associated with high morbidity and short-term and long-term mortality in all age groups worldwide. Pneumonia is broadly divided into community-acquired pneumonia or hospital-acquired pneumonia.[1]

The community-acquired pneumonia (CAP) is the leading cause of morbidity and mortality worldwide. According to WHO estimates, 450 million cases of pneumonia are recorded each year, with about 4 million deaths from this illness[2], with the highest incidence cases in children younger than 5 years old. The mortality rate has declined greatly due to early and accurate detection of the etiological agents, together with the timely initiation of appropriate treatment. BioFire FilmArray Pneumonia Panel plus (BFPP) is a simple multiplexed PCR system that integrates sample preparation, nucleic acid extraction, amplification, and analysis of microbial etiology, with a turnaround time of about one hour. In comparison to standard culture methods, BFPP is simpler, easier to perform, and can simultaneously detect the most common pathogens involved in lower respiratory tract infections.[3]

Improved infection control has reduced the NHS's burden of methicillin-resistant Staphylococcus aureus (MRSA) and Clostridium difficile, but resistance rates among Gram-negative bacteria are rising and, on an international basis, are doing so alarmingly, e.g. with an explosive increase of K. pneumoniae with KPC carbapenemases in Italy and Greece and Enterobacterales with NDM carbapenemases in the Indian subcontinent. Most carbapenemase producers are susceptible in vitro only to a few antibiotics, e.g. colistin and tigecycline, that have significant toxicity and efficacy limitations. Biofire film analysis will (i) compare the clinicians' decision-making with and without the FilmArray test, (ii) explore clinicians' barriers to adopting molecular diagnostics and (iii) provide evidence-based recommendations for how to overcome these.[4]

Severe CAP is a life-threatening condition defined by the presence of respiratory failure or symptoms of severe sepsis or septic shock. It accounts for approximately 10% of hospitalized patients with CAP. The majority of patients with severe pneumonia have underlying comorbid illnesses, with COPD, alcoholism, chronic heart disease, and diabetes mellitus being the most frequent. S. pneumoniae, Legionella spp, GNEB (especially K. pneumoniae), H. influenzae, S. aureus/spp, Mycoplasma pneumoniae, respiratory viruses (especially influenza viruses), and P. aeruginosa represent the most important causative organisms of severe CAP.[5]

The choice of empirical antibiotic treatment for sCAP depends on multiple factors, such as national and local antimicrobial susceptibility data and the characteristics of patients, including their risk factors for acquiring infections caused by MDR pathogens.[6]

Severity assessment tools may help clinicians recognise severe CAP and select patients for early intervention. In 1997, Fine et al. showed that the Pneumonia Severity Index (PSI) predicts mortality. This was followed by validation of the CURB65 (Confusion, Urea, Respiratory Rate, Blood pressure, Age > 65 years) score. However, while both the PSI and the CURB65 score guide decisions to hospitalise patients, they were not designed to guide ICU admission.[7]

6.2 REVIEW OF LITERATURE

S Jain, Self WH, et al. The EPIC study was a large, contemporary, prospective, population-based study of community-acquired pneumonia in hospitalized adults in the United States. The estimated incidences of hospitalization for pneumonia among adults 50 to 64 years of age, 65 to 79 years of age, and 80 years of age or older were approximately 4, 9, and 25 times as high, respectively, as the incidence among adults 18 to 49 years of age. Pathogens were detected in 38% of the patients, with viruses detected in 27% and bacteria in 14%. Human rhinovirus, influenza virus, and S. pneumoniae were the most commonly detected pathogens, with the highest burden occurring among older adults. The annual incidence of community-acquired pneumonia requiring hospitalization that they observed — 24.8 cases per 10,000 adults — is similar to the incidence of 26.7 cases per 10,000 adults that was observed in a prospective study conducted in Ohio in 1991. Methodologic differences in enrollment criteria, methodologic differences in incidence estimations, changes or differences in demographic characteristics, and changes in the provision of and access to health care preclude direct comparisons of incidence between the studies. Their estimates are lower than the rates of pneumonia requiring hospitalization that are based on claims data, owing to their exclusion of recently hospitalized or severely immunocompromised patients and the increased specificity of radiographic confirmation in their case definition.[8]

Musher DM, Roig IL, et al. Determining the cause of community-acquired pneumonia (CAP) remains problematic. In this observational study, they systematically applied currently approved diagnostic techniques in patients hospitalized for CAP in order to determine the proportion in which an etiological agent could be identified. By final clinical diagnosis, 44 patients (17.0%) were uninfected. A causative bacterium was identified in only 60 (23.2%) cases. PCR identified a respiratory virus in 42 (16.2%), 12 with documented bacterial coinfection. In 119 (45.9%), no cause for CAP was found; 69 (26.6%) of these had a syndrome indistinguishable from bacterial pneumonia.

Procalcitonin was elevated in patients with bacterial infection and low in uninfected patients or those with viral infection, but with substantial overlap.[9]

Gadsby NJ, Russell CD, et al. The frequent lack of a microbiological diagnosis in community-acquired pneumonia (CAP) impairs pathogen-directed antimicrobial therapy. This study assessed the use of comprehensive multibacterial, multiviral molecular testing, including quantification, in adults hospitalized with CAP. Comprehensive molecular testing of single lower respiratory tract (LRT) specimens achieved pathogen detection in 87% of CAP patients compared with 39% with culture-based methods. Haemophilus influenzae and Streptococcus pneumoniae were the main agents detected, along with a wide variety of typical and atypical pathogens. Viruses were present in 30% of cases; 82% of these were codetections with bacteria. Most (85%) patients had received antimicrobials in the 72 hours before admission. Of these, 78% had a bacterial pathogen detected by PCR but only 32% were culture-positive ($P < .0001$). Molecular testing had the potential to enable de-escalation in number and/or spectrum of antimicrobials in 77% of patients.[10]

Loeffelholz MJ, Pong DL, et al. They compared the diagnostic performance and overall respiratory pathogen detection rate of the premarket version of the FilmArray Respiratory Panel (RP) multiplex PCR assay (Idaho Technology, Inc., Salt Lake City, UT) with those of the Food and Drug Administration (FDA)-cleared Prodesse ProFlu+, ProFAST+, ProParaflu+, Pro hMPV+, and ProAdeno+ real-time PCR assays (Gen-Probe, San Diego, CA). The assays were performed on a panel of 192 nasopharyngeal-secretion specimens collected from 81 children under 1 year of age with upper respiratory tract symptoms. To resolve discordant results and confirm pathogens detected only by the larger FilmArray panel, they performed laboratory-developed real-time PCR assays. Among viruses detectable by both commercial assays (adenovirus, human metapneumovirus, influenza A virus, influenza B virus, parainfluenza viruses 1 to 3, and respiratory syncytial virus), the FilmArray and Prodesse assays showed good overall agreement

(181/192 [94.3%]; kappa = 0.87; 95% CI, 0.79 to 0.94). FilmArray RP detected more parainfluenza viruses 1 and 3 than ProParaflu+ (18 versus 13) while ProAdeno+ detected more adenoviruses (11 versus 6), but these differences were not statistically significant. Additionally, FilmArray RP detected 138 pathogens (confirmed as true positives) not included in the Prodesse assays (rhinovirus [RV]/enterovirus [EV], 118; bocavirus, 8; coronavirus, 7; parainfluenza virus 4, 4; Mycoplasma pneumoniae, 1). FilmArray RP was cleared by the FDA following the completion of this study. The FDA-cleared version includes the following targets: adenovirus, coronaviruses HKU1 and NL63, human metapneumovirus (hMPV), influenza A virus (to type level only), influenza A H1 seasonal virus, influenza A H3 seasonal virus, influenza A virus H1-2009, influenza B virus, parainfluenza viruses 1 to 4, respiratory syncytial virus (RSV), and RV/EV (no differentiation). The larger panel in the FilmArray RP assay allowed the detection of additional respiratory pathogens compared to the Prodesse assays. In this population of young children with upper respiratory tract infection, RV/EV accounted for the majority of the additional pathogens detected by FilmArray RP.[11]

Rand KH, Beal SG, et al. Antibiotic treatment decisions in severely ill patients must often be made in the absence of microbiologic results. The recently Food and Drug Administration–cleared BioFire FilmArray Pneumonia Panel (PN) detects 15 bacteria semiquantitatively, 3 atypical pneumonia bacteria, 8 viruses, and 7 antimicrobial resistance markers by multiplex PCR in ~1 hour in the laboratory. Previous reports have shown that the PN Panel bacterial detections are highly accurate, even when routine culture had no growth. Consecutive bronchoalveolar lavage and endotracheal specimens submitted for culture between June and September 2018 from 270 patients with sufficient clinical and laboratory data were tested with the PN Panel. Patients were divided into 3 groups: (1) both culture and PN Panel positive, (2) PN Panel positive but culture uninformative (no growth or normal flora), and (3) patients with no PN Panel detections.[12]

Gilbert DN, Leggett JE, et al. Although most observational studies identify viral or bacterial pathogens in 50% or less of patients hospitalized with community-acquired pneumonia (CAP), they previously demonstrated that a multi-test bundle (MTB) detected a potential pathogen in 73% of patients. This study compares detection rates for potential pathogens with the MTB versus the Biofire® Pneumonia FilmArray® panel (BPFA) multiplex PCR platform and presents an approach for integrating BPFA results as a foundation for subsequent antibiotic stewardship (AS) activities.[13]

Kosai K, Akamatsu N, et al. This study investigated the diagnostic utility of the BioFire FilmArray Pneumonia Panel (PN panel), an automated and multiplexed nucleic acid detection system that rapidly detects 26 pathogens (18 bacteria and eight viruses) and seven antimicrobial resistance markers in a single assay. They analyzed the targets in lower respiratory tract specimens using the PN panel and compared the detection results with those of bacterial culture methods and antimicrobial susceptibility testing. Of the 57 samples analyzed, the PN panel detected 97 targets (84 bacteria, four viruses, and nine antimicrobial resistance markers). Detection of bacteria and antimicrobial resistance was three times greater than that of the bacterial culture (25 bacteria and two resistant isolates) against the targets available in the panel. The overall positive and negative percent agreements between the PN panel and culture methods for bacterial detection were 100.0% and 92.9%, respectively. Multiple pathogens were detected by the PN panel in 24 samples (42.1%), ranging from two pathogens in 11 samples (19.3%) to six pathogens in one sample (1.8%). The PN panel semiquantitatively detected higher copies (≥ 106 copies/mL) of bacterial targets if the bacteria were positive by the culture method. In contrast, the semiquantitative values obtained by the panel varied (104 to 107 ≤ copies/mL) among bacteria that were negative by the culture method.[14]

6.3 AIMS AND OBJECTIVES OF THE STUDY

1. To compare the clinical significance of diagnosing pneumonia in patients with FilmArray versus those with standard methods.
2. To determine any difference in clinical cure of pneumonia between patients treated according to the FilmArray test's molecular results versus those treated with standard methods.
3. To determine whether there is an improvement in antimicrobial selection in pneumonia patients treated according to the FilmArray test versus those treated with standard methods.

7. MATERIALS AND METHODS

- Clinical Specimens. Taking ET secretions, BAL and sputum of hospitalized patients of DMCH Ludhiana.
- Multiplex Real-Time PCR Assay. The specimens collected from ET secretions, BAL, sputum were taken up for multiplex PCR pneumonia panel.
- Standard Methods- sputum for gram stain and culture sensitivity.

7.1 SOURCE OF DATA:

Hospitalised patients population who are having clinical features of pneumonia and X-ray changes.

7.2 METHOD OF COLLECTION OF DATA

- **Inclusion Criterion**

Include:

1) Hospitalized patients
2) In-patient in WARD/ICU/CCU
3) Breathing spontaneously or intubated
4) About to receive antibiotics for LRTI on admission
5) Have cardinal signs of pneumonia(new lung infiltrate, lobar consolidation, cavitation on chest xray, clinical evidence{fever, dyspnea, cough and sputum production})

- **Exclusion Criterion**

Includes:

1) All outpatients
2) Not consenting for study
3) Already started on antibiotics before admission in DMCH

DURATION OF STUDY/ NUMBER OF CASES

15th September 2022 to 15th September 2023

OUTCOME

To compare the difference between diagnosis, clinical cure and antimicrobial selection between those treated according to film array and others with standard methods.

STATISTICAL ANALYSIS (Name of the method in plan) Data will be described in terms of range; mean ±standard deviation (± SD), median, frequencies (number of cases) and relative frequencies (percentages) as appropriate. To determine whether the data is normally distributed, a Kolmogorov-Smirnov test will be used. For comparing categorical data, Chi square ($\chi 2$) test will be performed and fisher exact test will be used when the expected frequency is less than 5. The numbers of true-positive (TP), true-negative (TN), false-positive (FP), and false-negative (FN) results will be calculated A probability value (p value) less than 0.05 will be considered statistically significant. All statistical calculations will be done using (Statistical Package for the Social Science) SPSS 21version (SPSS Inc., Chicago, IL, USA) statistical program for Microsoft Windows. CROSS-SECTIONAL STUDY ANALYSIS.

7.3 DOES THE STUDY REQUIRE ANY INVESTIGATIONS OR INTERVENTIONS TO BE CONDUCTED ON PATIENTS OR OTHER HUMANS OR ANIMALS? IF SO, PLEASE DESCRIBE BRIEFLY.

Yes, routine investigations like CBC, RFTs, LFTs, urine routine and culture, blood culture, sputum sample analysis, ET secretions analysis, biofire film array.

7.4 HAS ETHICAL CLEARANCE BEEN OBTAINED FROM YOUR INSTITUTION IN CASE OF 7.3?

Yes, Attached herewith.

8. LIST OF REFERENCES

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PROFORMA

SR. NO.

PATIENT'S NAME:

AGE:

SEX:

ADDRESS:

MRD NO.:

DATE OF ADMISSION_____ DATE OF DISCHARGE_____

1. PRESENT ILLNESS:

2. COMORBIDITIES:

3. PERSONAL HISTORY:

4. OCCUPATION:

GENERAL PHYSICAL EXAMINATION:

PULSE:

BLOOD PRESSURE:

TEMPERATURE:

RESPIRATORY RATE:

PALLOR / CYANOSIS /CLUBBING / EDEMA/LYMPHADENOPATHY/ICTERUS

JVP

Signature of Candidate **Signature of Supervisor**

RESPIRATORY SYSTEM EXAMINATION:

INVESTIGATIONS:

ROUTINE

CHEST X-RAY

CT CHEST

METHOD: FILMARRAY

STANDARD METHODS: GRAM STAIN

CULTURE SENSITIVITY

SAMPLE: SPUTUM

ET SECRETION

BAL

FINDINGS: 1. BACTERIA

2. ATYPICAL BACTERIA

3. VIRUS

Signature of Candidate **Signature of Supervisor**

4. ANTIMICROBIAL RESISTANCE GENES

TREATMENT GIVEN:

OUTCOME

CLINICAL OUTCOME:

RADIOLOGICAL OUTCOME:

Signature of Candidate **Signature of Supervisor**

INFORMED PATIENT CONSENT

Date: _____

I…….D/o, W/o, S/o……..…… am willing to participate in the study **"ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA"** The procedure with its complications has been explained to me in local vernacular language. I have fully understood that no special tests and extra expenditure in any form, merely for the purpose of thesis is being carried out. I am free to opt out the study any time without assigning any reason.

……. ……
Signature of the Witness Signature of the patient

Name:

Signature of Candidate **Signature of Supervisor**

मरीज अनुमति फार्म

तिथि _____

मैं _____ पत्नी/पुत्र/पुत्री _____

निवासी _____

इस शोधकार्य **"ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA"** में भाग लेने के लिए सहमत हूँ। मैं इस शोधकार्य में भाग लेने के लिए अपनी स्वेच्छा से तैयार हूँ। मैं पुष्टि करता/करती हूँ की यह स्वीकृति देने के लिए मुझे कोई आर्थिक प्रलोभन नहीं दिया गया और न ही दबाव डाला गया है। मुझे इस शोधकार्य का उद्देश्य स्पष्ट कर दिया गया है और मुझे यह विश्वास है की यह विज्ञान और मानवता के लाभ के लिए है। मुझे इस शोधकार्य में होने वाले जोखिम के बारे में समझा दिया गया है और मेरी समझ में यह जोखिम बहुत मामुली है।

मैं इस शोधकार्य में भाग लेने के सम्बन्ध में किसी भी समय अपनी अस्वीकृति व्यक्त कर सकता/सकती हूँ और मेरे अस्वीकृति व्यक्त करने का मेरे इलाज पर कोई प्रभाव नहीं पड़ेगा।

_____	_____
गवाह के हस्ताक्षर	रोगी के हस्ताक्षर/अंगूठे का निशान
नाम:	नाम:

_____

अन्वेषक के हस्ताक्षर

_____

विद्यार्थी के हस्ताक्षर

ਮਰੀਜ਼ ਰਜ਼ਾਮੰਦੀ ਫਾਰਮ

ਮਿਤੀ_____

ਮੈ_____ਪਤਨੀ/ਪੁੱਤਰ/ਪੁੱਤਰੀ_____

ਵਾਸੀ _____

“ROLE OF MULTIPLEX PCR PNEUMONIA PANEL IN DETERMINING THE DIAGNOSIS, ANTIBIOTICS SELECTION AND OUTCOME IN PATIENTS WITH PNEUMONIA” ਤੇ ਚਲ ਰਹੀ ਖੋਜ ਵਿਚ ਹਿੱਸਾ ਲੈਣ ਲਈ ਰਜ਼ਾਮੰਦ ਹਾਂ। ਇਸ ਖੋਜ ਕੰਮ ਵਿਚ ਹਿੱਸਾ ਲੈਣ ਲਈ ਮੈ ਆਪਣੀ ਮਰਜ਼ੀ ਨਾਲ ਤਿਆਰ ਹਾਂ। ਮੈ ਇਹ ਦਸਣਾ ਚਾਹੁੰਦਾ ਹਾਂ/ ਚਾਹੁੰਦੀ ਹਾਂ ਕੇ ਇਹ ਰਜ਼ਾਮੰਦੀ ਦੇਣ ਵਾਸਤੇ ਮੈਨੂ ਕਿਸੇ ਵੀ ਤਰਾਂ ਦਾ ਲੋਭ-ਲਾਲਚ ਨਹੀ ਦਿੱਤਾ ਗਿਆ ਅਤੇ ਨਾ ਹੀ ਕੋਈ ਦਬਾ ਪਾਇਆ ਗਿਆ ਹੈ। ਮੈਨੂ ਇਸ ਖੋਜ ਦਾ ਮਨੋਰਥ ਸਮਝਾ ਦਿੱਤਾ ਗਿਆ ਹੈ ਅਤੇ ਮੈਨੂ ਇਹ ਭਰੋਸਾ ਦਵਾਇਆ ਗਿਆ ਹੈ ਕੇ ਇਹ ਖੋਜ ਵਿਗਿਆਨ ਅਤੇ ਮਾਨਵਤਾ ਦੀ ਭਲਾਈ ਲਈ ਹੈ। ਮੈਨੂ ਇਸ ਖੋਜ ਵਿਚ ਹੋਣ ਵਾਲੇ ਖਤਰੇ ਬਾਰੇ ਸਮਝਾ ਦਿੱਤਾ ਗਿਆ ਹੈ ਅਤੇ ਮੈਨੂ ਇਹ ਯਕੀਨ ਹੈ ਕੇ ਇਹ ਖਤਰਾ ਬਹੁਤ ਮਾਮੂਲੀ ਹੈ। ਮੈਨੂ ਇਸ ਖੋਜ ਕੰਮ ਵਿਚ ਹਿੱਸਾ ਲੈਣ ਦਾ ਢੰਗ – ਤਰੀਕਾ ਸਮਝਾ ਦਿੱਤਾ ਗਿਆ ਹੈ।

ਮੈ ਇਸ ਖੋਜ ਕੰਮ ਵਿਚ ਹਿੱਸਾ ਲੈਣ ਬਾਰੇ ਆਪਣੀ ਰਜ਼ਾਮੰਦੀ ਕਿਸੇ ਵੀ ਸਮੇ ਵਾਪਸ ਲੈ ਸਕਦਾ ਹਾਂ/ ਸਕਦੀ ਹਾਂ ਅਤੇ ਮੇਰੀ ਰਜ਼ਾਮੰਦੀ ਵਾਪਸ ਲੈਣ ਦਾ ਮੇਰੇ ਇਲਾਜ ਤੇ ਕੋਈ ਅਸਰ ਨਹੀ ਹੋਵੇਗਾ।

_____	_____
ਗਵਾਹ ਦੇ ਹਸਤਾਖਰ	ਮਰੀਜ਼ ਦੇ ਹਸਤਾਖਰ
ਮਿਤੀ_____	ਮਿਤੀ_____
ਪਤਾ _____	ਪਤਾ _____

_____
ਨਿਰੀਖਕ ਦੇ ਹਸਤਾਖਰ

_____
ਸਿਖਿਆਰਥੀ ਦੇ ਹਸਤਾਖਰ